

FILE 'HCAPLUS' ENTERED AT 13:42:39 ON 10 JUN 2010

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L1      1369 S BRANCHING ENZYME
L2      44820 S MAIZE
L3      263 S L1 AND L2
L4      96 S L3 AND (PY<2000 OR AY<2000 OR PRY<2000)
L5      808 S (BRANCHING ENZYME) (4A) (STARCH)
L6      851 S (BRANCHING ENZYME) (4A) (STARCH OR AMYLOSE OR AMYLOPECTIN)
L7      231 S L2 AND L6
L8      71 S L7 AND (PY<2000 OR AY<2000 OR PRY<2000)
L9      2911043 S EXPRESSION OR EXPRESSED OR (DEGREE OF BRANCHING) OR (BRANCHIN
L10     60 S L8 AND L9
L11     1540936 S EXPRESSION OR EXPRESSED OR (DEGREE OF BRANCHING) OR (BRANCHIN
L12     33 S L8 AND L11
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HCAplus now includes complete International Patent Classification (IPC) reclassification data for the second quarter of 2010.

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<http://www.cas.org/legal/infopolicy.html>

This file contains CAS Registry Numbers for easy and accurate substance identification.

```
=> s branching enzyme
      65463 BRANCHING
      937081 ENZYME
L1      1369 BRANCHING ENZYME
          (BRANCHING(W)ENZYME)
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=> s algae or algal or reinhardtii or reinhardtii
      55914 ALGAE
      24232 ALGAL
          1 REINHARDTT
          2734 REINHARDTII
L2      69842 ALGAE OR ALGAL OR REINHARDTT OR REINHARDTII
```

```
=> s l1 and l2
L3      22 L1 AND L2
```

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=> d l3 1-22 ti abs bib
```

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L3      ANSWER 1 OF 22 HCAPLUS COPYRIGHT 2010 ACS on STN
TI      Starch biosynthesis in plants
AB      A review. Starch is a major storage compound in plants that is present both
in leaves and in storage tissues. Biochem. and mol. biol. data show that
ADP-glucose is the glucosyl donor for plant starch synthesis, and its
synthesis is catalyzed by ADP-glucose pyrophosphorylase. Subsequently,
starch synthases catalyze the transfer of the glucosyl residue from
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ADP-glucose to the oligosaccharide chains of the starch components amylose and amylopectin to form new  $\alpha$ -1,4-glucosidic residues. After elongation of these  $\alpha$ -1,4-glucosidic chains, the branching enzyme catalyzes a cleavage of the elongated chain and transfers the cleaved portion of the oligosaccharide chain to either another region in the amylopectin mol. or to a new amylopectin and forms a new  $\alpha$ -1,6-glucosidic linkage. Amylose synthesis is catalyzed by the granule-bound starch synthase. Regulation of starch synthesis occurs at the ADP-glucose pyrophosphorylase step. The enzyme from higher plants, green algae, and cyanobacteria is activated allosterically by 3-phosphoglycerate and inhibited by inorg. phosphate. Isolation of mutants and control analyses indicate that the allosteric activation and inhibition are of physiol. and functional importance in the regulation of starch synthesis. Furthermore, evidence indicates that ADP-glucose pyrophosphorylases can also be regulated by a redox mechanism. The current knowledge of the enzyme structures and critical amino acids necessary for substrate binding, allosteric effector binding, regulation, and catalysis for the ADP-glucose pyrophosphorylase is reviewed.

AN 2009:1026885 HCAPLUS <<LOGINID::20100610>>

DN 152:376834

TI Starch biosynthesis in plants

AU Preiss, Jack

CS Department of Biochemistry and Molecular Biology, Michigan State University, East Lansing, MI, USA

SO Wiley Encyclopedia of Chemical Biology (2009), Volume 4, 362-376.

Editor(s): Begley, Tadhg P. Publisher: John Wiley & Sons, Inc., Hoboken, N. J.

CODEN: 69LUOU; ISBN: 978-0-471-75477-0

DT Conference; General Review

LA English

RE.CNT 144 THERE ARE 144 CITED REFERENCES AVAILABLE FOR THIS RECORD  
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L3 ANSWER 2 OF 22 HCAPLUS COPYRIGHT 2010 ACS on STN

TI Chlorella starch branching enzyme II (BEII) can  
complement the function of BEIIb in rice endosperm

AB In monocots, starch branching enzyme II (BEII) was functionally differentiated into BEIIa and BEIIb after separation from the dicots, and in cereals BEIIb plays a distinct role in amylopectin biosynthesis in the endosperm. The present study was conducted to examine to what extent a green algal BEII has an overlapping function with BEIIb in starch biosynthesis by introducing the Chlorella BEII gene into an amylose-extender (ae) mutant of rice. Chlorella BEII was found to complement the contribution of the rice endosperm BEIIb to the structures of amylopectin and starch granules because these mutated phenotypes were recovered almost completely to those of the wild type by the expression of Chlorella BEII. When the recombinant BE enzymes were incubated with the rice ae amylopectin, the branching pattern of Chlorella BEII was much more similar to that of rice BEIIb rather than rice BEIIa. Detailed analyses of BE reaction products suggests that BEIIb and Chlorella BEII only transfer chains with a d.p. (DP) of 6 and 7, whereas BEIIa preferably transfers short chains with a DP of about 6-11. These results show that the Chlorella BEII is functionally similar to rice BEIIb rather than BEIIa.

AN 2009:735243 HCAPLUS <<LOGINID::20100610>>

DN 151:354291

TI Chlorella starch branching enzyme II (BEII) can  
complement the function of BEIIb in rice endosperm

AU Sawada, Takayuki; Francisco, Perigio B., Jr.; Aihara, Satomi; Utsumi, Yoshinori; Yoshida, Mayumi; Oyama, Yasunori; Tsuzuki, Mikio; Satoh, Hikaru; Nakamura, Yasunori

CS CREST, Japan Science and Technology Corporation, Kawaguchi, Saitama,  
332-0012, Japan  
SO Plant and Cell Physiology (2009), 50(6), 1062-1074  
CODEN: PCPHA5; ISSN: 0032-0781  
PB Oxford University Press  
DT Journal  
LA English

RE.CNT 38 THERE ARE 38 CITED REFERENCES AVAILABLE FOR THIS RECORD  
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L3 ANSWER 3 OF 22 HCAPLUS COPYRIGHT 2010 ACS on STN  
TI Manufacture of branched carbohydrate using branching  
enzyme and application in food  
AB Branched  $\alpha$ -glucan of (d.p., 5-15) is manufactured from  
 $\alpha$ -glucan-containing starch hydrolyzate with branching  
enzyme such as  $\alpha$ -amylase. The branching  
enzyme is obtained from rice, corn, potato, algae, etc.  
The branched  $\alpha$ -glucan is useful for making food such as syrup.  
AN 2009:701978 HCAPLUS <<LOGINID::20100610>>  
DN 150:562162  
TI Manufacture of branched carbohydrate using branching  
enzyme and application in food  
IN Ohata, Yuichiro; Yamamoto, Takeshi; Nakamura, Yasunori; Fujita, Naoko;  
Nakakuki, Teruo  
PA Akita Prefectural University, Japan; Nihon Shokuhin Kako Co., Ltd.  
SO Jpn. Kokai Tokkyo Koho, 15pp.  
CODEN: JKXXAF  
DT Patent  
LA Japanese

FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
	-----	----	-----	-----	-----
PI	JP 2009124994	A	20090611	JP 2007-303256	20071122
PRAI	JP 2007-303256		20071122		

L3 ANSWER 4 OF 22 HCAPLUS COPYRIGHT 2010 ACS on STN  
TI The phenotype of soluble starch synthase IV defective mutants of  
Arabidopsis thaliana suggests a novel function of elongation enzymes in  
the control of starch granule formation  
AB All plants and green algae synthesize starch through the action  
of the same five classes of elongation enzymes: the starch synthases.  
Arabidopsis mutants defective for the synthesis of the soluble starch  
synthase IV (SSIV) type of elongation enzyme have now been characterized.  
The mutant plants displayed a severe growth defect but nonetheless  
accumulated near to normal levels of polysaccharide storage. Detailed  
structural anal. has failed to yield any change in starch granule  
structure. However, the number of granules per plastid has dramatically  
decreased leading to a large increase in their size. These results, which  
distinguish the SSIV mutants from all other mutants reported to date,  
suggest a specific function of this enzyme class in the control of granule  
nos. We speculate therefore that SSIV could be selectively involved in  
the priming of starch granule formation.  
AN 2007:248135 HCAPLUS <<LOGINID::20100610>>  
DN 147:5811  
TI The phenotype of soluble starch synthase IV defective mutants of  
Arabidopsis thaliana suggests a novel function of elongation enzymes in  
the control of starch granule formation  
AU Roldan, Isaac; Wattebled, Fabrice; Lucas, M. Mercedes; Delvalle, David;  
Planchot, Veronique; Jimenez, Sebastian; Perez, Ricardo; Ball, Steven;  
D'Hulst, Christophe; Merida, Angel  
CS Instituto de Bioquimica Vegetal y Fotosintesis, CSIC-US, Seville, 41092,

Spain

SO Plant Journal (2007), 49(3), 492-504  
CODEN: PLJUED; ISSN: 0960-7412

PB Blackwell Publishing Ltd.

DT Journal

LA English

OSC.G 21 THERE ARE 21 CAPLUS RECORDS THAT CITE THIS RECORD (21 CITINGS)

RE.CNT 45 THERE ARE 45 CITED REFERENCES AVAILABLE FOR THIS RECORD  
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L3 ANSWER 5 OF 22 HCAPLUS COPYRIGHT 2010 ACS on STN

TI Common evolutionary origin of starch biosynthetic enzymes in green and red algae

AB Plastidic starch synthesis in green algae and plants occurs via ADP-glucose in likeness to prokaryotes from which plastids have evolved. In contrast, floridean starch synthesis in red algae proceeds via uridine diphosphate-glucose in semblance to eukaryotic glycogen synthesis and occurs in the cytosol rather than the plastid. Given the monophyletic origin of all plastids, we investigated the origin of the enzymes of the plastid and cytosolic starch synthetic pathways to determine whether their location reflects their origin-either from the cyanobacterial endosymbiont or from the eukaryotic host. We report that, despite the compartmentalization of starch synthesis differing in green and red lineages, all but one of the enzymes of the synthetic pathways shares a common origin. Overall, the pathway of starch synthesis in both lineages represents a chimera of the host and endosymbiont glycogen synthesis pathways. Moreover, host-derived proteins function in the plastid in green algae, whereas endosymbiont-derived proteins function in the cytosol in red algae. This complexity demonstrates the impacts of integrating pathways of host with those of both primary and secondary endosymbionts during plastid evolution.

AN 2006:69305 HCAPLUS <<LOGINID::20100610>>

DN 145:392317

TI Common evolutionary origin of starch biosynthetic enzymes in green and red algae

AU Patron, Nicola J.; Keeling, Patrick J.

CS Canadian Institute for Advanced Research, Botany Department, University of British Columbia, Vancouver, BC, V6T 1Z4, Can.

SO Journal of Phycology (2005), 41(6), 1131-1141  
CODEN: JPYLAJ; ISSN: 0022-3646

PB Blackwell Publishing, Inc.

DT Journal

LA English

OSC.G 21 THERE ARE 21 CAPLUS RECORDS THAT CITE THIS RECORD (21 CITINGS)

RE.CNT 75 THERE ARE 75 CITED REFERENCES AVAILABLE FOR THIS RECORD  
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L3 ANSWER 6 OF 22 HCAPLUS COPYRIGHT 2010 ACS on STN

TI Polyglucan synthase gene knockout Cyanobacterium and use in screening the effects of heterologous genes on  $\alpha$ -polyglucan biosynthesis

AB Polyglucan synthase gene knockout blue-green algae and use in screening the effects of heterologous genes on  $\alpha$ -polyglucan biosynthesis, is disclosed. Cyanobacterium *Synechococcus* sp. PCC7942 deficient in the gene coding for glycogen synthase (GS), glycogen branching enzyme (BE), or isoamylase (ISA), were generated.

AN 2004:819634 HCAPLUS <<LOGINID::20100610>>

DN 141:308640

TI Polyglucan synthase gene knockout Cyanobacterium and use in screening the effects of heterologous genes on  $\alpha$ -polyglucan biosynthesis

IN Suzuki, Eiji; Moriya, Katsuya; Takahashi, Junichiro; Kudo, Haruka;

Nakamura, Yasunori  
 PA Japan Science and Technology Agency, Japan  
 SO Jpn. Kokai Tokkyo Koho, 99 pp.  
 CODEN: JKXXAF  
 DT Patent  
 LA Japanese  
 FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	JP 2004275050	A	20041007	JP 2003-69795	20030314
	JP 4267942	B2	20090527		
PRAI	JP 2003-69795		20030314		

L3 ANSWER 7 OF 22 HCAPLUS COPYRIGHT 2010 ACS on STN  
 TI A transformed plant having a reduced endogenous starch branching enzyme activity and a heterologous glucan branching enzyme and its use for production of starch  
 AB The present invention relates to a transformed plant having a reduced endogenous starch branching enzyme (SBE) activity, and having a heterologous glucan branching enzyme (GBE) activity. The invention also relates to starch obtainable from such a plant. Reduction of potato SBE activity by antisense SBE I and SBE II expression is described. Cloning and sequencing of SBE from the red alga Gracilaria lemaneiformis and heterologous expression of the enzyme in potato tubers are reported. Gene, and encoded amino acid sequences of the G. lemaneiformis SBE are disclosed. Heterologous expression of a glycogen branching enzyme from E. coli in potato tubers is described. Production of floridean-starch types and glycogen-starch types in transgenic potatoes using the heterologously expressed G. lemaneiformis SBE and glycogen branching enzyme from E. coli resp. is described.

AN 2001:713525 HCAPLUS <<LOGINID::20100610>>  
 DN 135:268185  
 TI A transformed plant having a reduced endogenous starch branching enzyme activity and a heterologous glucan branching enzyme and its use for production of starch  
 IN Poulson, Peter; Sorensen, Iben Schildt  
 PA Danisco A/s, Den.  
 SO PCT Int. Appl., 51 pp.  
 CODEN: PIXXD2  
 DT Patent  
 LA English  
 FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2001070942	A2	20010927	WO 2001-IB493	20010316
	WO 2001070942	A3	20020404		
	W:	AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW			
	RW:	GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG			
GB	2360521	A	20010926	GB 2000-6733	20000320
CA	2402463	A1	20010927	CA 2001-2402463	20010316
EP	1265477	A2	20021218	EP 2001-914128	20010316
	R:	AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR			

US 20040068766 A1 20040408 US 2003-239145 20030115  
 PRAI GB 2000-6733 A 20000320  
 WO 2001-IB493 W 20010316

OSC.G 3 THERE ARE 3 CAPLUS RECORDS THAT CITE THIS RECORD (3 CITINGS)

RE.CNT 4 THERE ARE 4 CITED REFERENCES AVAILABLE FOR THIS RECORD

ALL CITATIONS AVAILABLE IN THE RE FORMAT

L3 ANSWER 8 OF 22 HCAPLUS COPYRIGHT 2010 ACS on STN

TI Fusion proteins with Chlamydomonas starch synthase and food and pharmaceuticals containing starch-fusion protein complexes

AB The invention concerns starch granules containing a hybrid protein between a starch synthase and a protein of interest, the nucleotide sequences used for obtaining same, methods for preparing them and their uses, particularly in pharmaceutical compns. Thus, the cDNA for the STA2 gene starch synthase of C. reinhardtii was cloned and sequenced. A C-terminal-truncated starch synthase of 58 kilodaltons (wild-type enzyme: 76 kilodaltons) encoded by the sta2-1 allele was found to have a six-fold increased Km for ADP-glucose and to bind to starch grains with unaltered affinity.

AN 2000:842295 HCAPLUS <<LOGINID::20100610>>

DN 134:14733

TI Fusion proteins with Chlamydomonas starch synthase and food and pharmaceuticals containing starch-fusion protein complexes

IN D'Hulst, Christophe; Ball, Steven

PA Centre National de la Recherche Scientifique, Fr.

SO PCT Int. Appl., 90 pp.

CODEN: PIXXD2

DT Patent

LA French

FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2000071734	A1	20001130	WO 2000-FR1384	20000519
	W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW				
	RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
	FR 2793806	A1	20001124	FR 1999-6494	19990521
	FR 2793806	B1	20030425		
	CA 2374416	A1	20001130	CA 2000-2374416	20000519
	EP 1179078	A1	20020213	EP 2000-929649	20000519
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO				
	JP 2003500060	T	20030107	JP 2000-620111	20000519
	US 6982083	B1	20060103	US 2002-980771	20020110
PRAI	FR 1999-6494	A	19990521		
	WO 2000-FR1384	W	20000519		

ASSIGNMENT HISTORY FOR US PATENT AVAILABLE IN LSUS DISPLAY FORMAT

OSC.G 2 THERE ARE 2 CAPLUS RECORDS THAT CITE THIS RECORD (2 CITINGS)

RE.CNT 9 THERE ARE 9 CITED REFERENCES AVAILABLE FOR THIS RECORD

ALL CITATIONS AVAILABLE IN THE RE FORMAT

L3 ANSWER 9 OF 22 HCAPLUS COPYRIGHT 2010 ACS on STN

TI Modified starch metabolism enzymes and encoding genes for improvement and optimization of plant phenotypes

AB The invention provides methods for generating, identifying, and selecting

polynucleotides encoding novel starch metabolizing enzymes (NSME), NSME-encoding polynucleotides, compns. of recombinant shuffled NSME protein, plant cells and microbes containing a shuffled NSME polynucleotide in expressible form, plants containing a shuffled NSME polynucleotide in expressible form, novel starch compns. produced by said plants and cells, uses of such plants, cells, and starch compns. Thus, to create an ADP-glucose pyrophosphorylase with altered properties, the genes from E. coli and other microorganisms which have at least 70% sequence identity are randomly fragmented with DNase I and fragments of 100-300 bp are selected. These fragments are reassembled based on sequence similarity by primerless PCR. Recombination as well as variable levels of mutations that are introduced by the PCR reaction to generate the diversity. The assembled genes are cloned into a starch minus E. coli mutant that lacks the NSME. Transformed colonies expressing a functional NSME are screened for production of glycogen by iodine staining. Those colonies staining dark blue are presumed to contain deregulated NSME. Colonies expressing shuffled NSME genes are selected and grown in larger amts. in liquid culture and assayed for specific properties. Genes from those clones expressing one or more of the desired properties are iteratively shuffled in order to achieve optimization of one or more of the desired properties. The optimized gene is used to transform the desired crop plant in order to deregulate and increase starch biosynthesis in various tissues including tubers and seeds.

AN 2000:742226 HCAPLUS <<LOGINID::20100610>>  
 DN 133:291931  
 TI Modified starch metabolism enzymes and encoding genes for improvement and optimization of plant phenotypes  
 IN Stemmer, Willem P. C.; Subramanian, Venkiteswaran; Raillard, Sun Ai; Huisman, Gjalt  
 PA Maxygen, Inc., USA  
 SO PCT Int. Appl., 71 pp.  
 CODEN: PIXXD2  
 DT Patent  
 LA English  
 FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2000061731	A2	20001019	WO 2000-US9840	20000412
	WO 2000061731	A3	20010222		
	W:	AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW			
	RW:	GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG			
	US 6703240	B1	20040309	US 2000-547844	20000412
PRAI	US 1999-129009P	P	19990413		

ASSIGNMENT HISTORY FOR US PATENT AVAILABLE IN LSUS DISPLAY FORMAT  
 OSC.G 2 THERE ARE 2 CAPLUS RECORDS THAT CITE THIS RECORD (2 CITINGS)  
 RE.CNT 6 THERE ARE 6 CITED REFERENCES AVAILABLE FOR THIS RECORD  
 ALL CITATIONS AVAILABLE IN THE RE FORMAT

L3 ANSWER 10 OF 22 HCAPLUS COPYRIGHT 2010 ACS on STN  
 TI Chimeric glycogen synthase gene-expressing transgenic plants with reduced starch loss at elevated growth temperature  
 AB Starch yield of wheat and maize plants grown under higher temps. than control plants is increased by the introduction of a chimeric gene comprising a glycogen synthase coding sequence under the control of a promoter directing expression and a terminator. A transit peptide for



translocation of the glycogen synthase to the plant plastid may also be included in the chimeric gene. The starch may also have altered processing characteristics, in particular an increased chain length. Thus, transgenic wheat and maize expressing a chimeric Escherichia coli glgA gene were produced. The chimeric gene consisted of the endosperm-specific high-mol.-weight glutenin gene promoter of wheat fused to the pea Rubisco small subunit transit peptide sequence fused to the glgA gene. Starch produced by these transgenic plants had an increased chain length. Addnl., seeds from these plants loss 8-11% less seed weight at 27° than did control plants.

AN 2000:666884 HCAPLUS <<LOGINID::20100610>>

DN 133:249926

TI Chimeric glycogen synthase gene-expressing transgenic plants with reduced starch loss at elevated growth temperature

IN Burrell, Michael Meyrick; Hedley, Clare

PA Advanced Technologies (Cambridge) Limited, UK

SO PCT Int. Appl., 76 pp.

CODEN: PIXXD2

DT Patent

LA English

FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2000055331	A1	20000921	WO 2000-GB848	20000309
	W:	AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW			
	RW:	GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG			
	CA 2365279	A1	20000921	CA 2000-2365279	20000309
	EP 1165802	A1	20020102	EP 2000-907849	20000309
	R:	AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO			
PRAI	GB 1999-5698	A	19990312		
	WO 2000-GB848	W	20000309		
OSC.G	1	THERE ARE 1 CAPLUS RECORDS THAT CITE THIS RECORD (1 CITINGS)			
RE.CNT	3	THERE ARE 3 CITED REFERENCES AVAILABLE FOR THIS RECORD			
		ALL CITATIONS AVAILABLE IN THE RE FORMAT			

L3 ANSWER 11 OF 22 HCAPLUS COPYRIGHT 2010 ACS on STN

TI Biosynthesis of altered starch in genetically modified plants with glycogen branching enzyme gene

AB A method and compns. for altering starch properties in wheat and maize plants, starch obtained by such method, and transgenic plants producing such starch, are disclosed. Starch with altered properties is produced by introducing a gene construct comprising a glycogen branching enzyme coding sequence under the control of a promoter directing expression and a terminator. A transit peptide for translocation of the glycogen branching enzyme to the plant plastid may also be included in the chimeric gene construct. The starch has altered processing characteristics, in particular an decreased chain length. A chimeric gene containing the High Mol. Weight Glutenin (HMWG) promoter, nopaline

synthase terminator, and the transit-peptide region of the small-subunit of the ribulose biphosphate carboxylase (ssu of Rubisco) gene was utilized to direct expression of Escherichia coli glycogen branching enzyme (glgB) to wheat and maize. Expression of the glgB gene product in wheat and maize grain was detected by

immunoblot anal. Anal. of the starch from these transgenic wheat and maize lines indicated an decrease in chain length, particularly an increase in chain length between 5 and 8 glucose units. The above parameters indicate a novel wheat and maize starch based on expression of the glgB E. coli gene product in transgenic plants.

AN 2000:368616 HCAPLUS <<LOGINID::20100610>>

DN 133:29689

TI Biosynthesis of altered starch in genetically modified plants with glycogen branching enzyme gene

IN Burrell, Michael Meyrick

PA Advanced Technologies (Cambridge) Limited, UK

SO PCT Int. Appl., 56 pp.

CODEN: PIXXD2

DT Patent

LA English

FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2000031282	A1	20000602	WO 1999-GB3762	19991108
	W:	AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, EE, ES, FI, GB, GE, GH, GM, HR, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, UZ, VN, YU, ZA, ZW			
	RW:	GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG			

PRAI GB 1998-25262 A 19981119

OSC.G 1 THERE ARE 1 CAPLUS RECORDS THAT CITE THIS RECORD (1 CITINGS)

RE.CNT 8 THERE ARE 8 CITED REFERENCES AVAILABLE FOR THIS RECORD

ALL CITATIONS AVAILABLE IN THE RE FORMAT

L3 ANSWER 12 OF 22 HCAPLUS COPYRIGHT 2010 ACS on STN

TI Biosynthesis of altered starch in genetically modified plants with glycogen synthase gene

AB A method and compns. for altering starch properties in wheat and maize plants , starch obtained by such method, and transgenic plants producing such starch, are disclosed. Starch with altered properties is produced by introducing a gene construct comprising a glycogen synthase coding sequence under the control of a promoter directing expression and a terminator. A transit peptide for translocation of the glycogen synthase to the plant plastid may also be included in the chimeric gene construct. The starch has altered processing characteristics, in particular an increased chain length. A chimeric gene containing the High Mol. Weight

Glutenin

(HMGW) promoter, nopaline synthase terminator, and the transit-peptide region of the small-subunit of the ribulose biphosphate carboxylase (ssu of Rubisco) gene was utilized to direct expression of Escherichia coli glycogen synthase (glgA) to wheat and maize. Expression of the glgA gene product in wheat and maize grain was detected by immunoblot anal. Anal. of the starch from these transgenic wheat and maize lines indicated an increase in chain length, particularly in chain length between 17 and 28 glucose units. Rapid viscometric anal. yielded lower peak and final viscosity values (about 30% of control values), whereas differential scanning calorimetry values indicated increased enthalpy values. The above parameters indicate a novel wheat and maize starch based on expression of the glgA E. coli gene product in transgenic plants.

AN 2000:368603 HCAPLUS <<LOGINID::20100610>>

DN 133:29688

TI Biosynthesis of altered starch in genetically modified plants with glycogen synthase gene

IN Burrell, Michael Meyrick  
 PA Advanced Technologies (Cambridge) Limited, UK  
 SO PCT Int. Appl., 66 pp.  
 CODEN: PIXXD2  
 DT Patent  
 LA English  
 FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2000031274	A1	20000602	WO 1999-GB3734	19991109
	W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, EE, ES, FI, GB, GE, GH, GM, HR, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, UZ, VN, YU, ZA, ZW				
	RW: GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
	CA 2349819	A1	20000602	CA 1999-2349819	19991109
	CA 2349819	C	20080909		
	EP 1131442	A1	20010912	EP 1999-954197	19991109
	EP 1131442	B1	20100526		
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, CY				
	US 6468799	B1	20021022	US 1999-444728	19991118
	AU 2000010616	A	20000807	AU 2000-10616	20000119
	AU 2004202150	A1	20040617	AU 2004-202150	20040519
	AU 2004202150	B2	20060713		
PRAI	GB 1998-25242	A	19981119		
	WO 1999-GB3734	W	19991109		
	AU 2000-10616	A3	20000119		

ASSIGNMENT HISTORY FOR US PATENT AVAILABLE IN LSUS DISPLAY FORMAT  
 OSC.G 2 THERE ARE 2 CAPLUS RECORDS THAT CITE THIS RECORD (2 CITINGS)  
 RE.CNT 7 THERE ARE 7 CITED REFERENCES AVAILABLE FOR THIS RECORD  
 ALL CITATIONS AVAILABLE IN THE RE FORMAT

L3 ANSWER 13 OF 22 HCAPLUS COPYRIGHT 2010 ACS on STN  
 TI Method for the preparation of a mixture of starch branching enzymes using a mutant of the green algae *Chlamydomonas reinhardtii*  
 AB The invention concerns a method for obtaining a mixture of starch branching enzymes extracted from unicellular algae characterized in that it consists in modifying a unicellular algae such that it no longer expresses a starch debranching activity; in treating said modified unicellular algae so as to obtain a concentrated acellular extract; and in subjecting said concentrated acellular extract to mol. sieving so as to obtain a mixture of starch branching enzymes extracted from algae. Thus the wild type green algae *Chlamydomonas reinhardtii* was mutated on the sta7 locus by inserting the pARG7 plasmid carrying the argininosuccinate lyase coding sequence. The obtained phenotype was lacking starch debranching enzyme activity. The mutant was used for fermentation in 10 L scale to produce starch branching enzymes I and II. After cell disruption in a French press, the extract was purified in several steps and used for amylopectin modification.  
 AN 2000:227757 HCAPLUS <<LOGINID::20100610>>  
 DN 132:235980  
 TI Method for the preparation of a mixture of starch branching enzymes using a mutant of the green algae *Chlamydomonas reinhardtii*  
 IN Fleche, Guy; Looten, Philippe; Heysen, Arnaud; Ball, Steven  
 PA Roquette Freres, Fr.  
 SO PCT Int. Appl., 29 pp.

CODEN: PIXXD2

DT Patent

LA French

FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2000018893	A1	20000406	WO 1999-FR2261	19990923
	W:	AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW			
	RW:	GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG			
	FR 2783838	A1	20000331	FR 1998-12051	19980925
	FR 2783838	B1	20001201		
	CA 2345331	A1	20000406	CA 1999-2345331	19990923
	AU 9956320	A	20000417	AU 1999-56320	19990923
	EP 1115843	A1	20010718	EP 1999-943032	19990923
	R:	AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO			
PRAI	FR 1998-12051	A	19980925		
	WO 1999-FR2261	W	19990923		
OSC.G	3	THERE ARE 3 CAPLUS RECORDS THAT CITE THIS RECORD (3 CITINGS)			
RE.CNT	4	THERE ARE 4 CITED REFERENCES AVAILABLE FOR THIS RECORD			
		ALL CITATIONS AVAILABLE IN THE RE FORMAT			

L3 ANSWER 14 OF 22 HCAPLUS COPYRIGHT 2010 ACS on STN

TI Cloning and characterization of a nuclear gene encoding a starch-branching enzyme from the marine red alga *Gracilaria gracilis*

AB The biosynthesis of starch in red algae occurs in the cytosol, in contrast to green plants where it takes place in the plastid. We have cloned a nuclear gene from the red alga *Gracilaria gracilis* that encodes a homolog of starch-branching enzymes (SBEs); this gene, which is apparently intron-free, was designated as GgSBE1. A potential TATA box, CAAT boxes, and other potential regulatory elements were observed in its 5' flanking region. The encoded 766-aa peptide shares significant sequence similarity with SBEs from green plants (at least 40%), and with glycogen-branching enzymes (GBEs) from human (46%) and *Saccharomyces cerevisiae* (45%). Southern-hybridization anal. indicates that the gene is single-copy, although weaker signals suggest that related genes exist in the genome of *G. gracilis*. Phylogenetic analyses indicate that GgSBE1 groups within the eukaryote branching enzymes (BEs) and not with eubacterial GBEs, suggesting that its gene has not been derived directly from an endosymbiotic cyanobacterium, but instead is ancestrally eukaryotic.

AN 1998:549701 HCAPLUS <<LOGINID::20100610>>

DN 130:972

TI Cloning and characterization of a nuclear gene encoding a starch-branching enzyme from the marine red alga *Gracilaria gracilis*

AU Lluisma, A. O.; Ragan, M. A.

CS Institute for Marine Biosciences, National Research Council of Canada, Halifax, NS, B3H 3Z1, Can.

SO Current Genetics (1998), 34(2), 105-111  
CODEN: CUGED5; ISSN: 0172-8083

PB Springer-Verlag

DT Journal

LA English

OSC.G 14 THERE ARE 14 CAPLUS RECORDS THAT CITE THIS RECORD (14 CITINGS)

RE.CNT 41        THERE ARE 41 CITED REFERENCES AVAILABLE FOR THIS RECORD  
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L3     ANSWER 15 OF 22   HCAPLUS   COPYRIGHT 2010 ACS on STN

TI     A Chlamydomonas reinhardtii low-starch mutant is defective for  
3-phosphoglycerate activation and orthophosphate inhibition of ADP-glucose  
pyrophosphorylase

AB     A low-starch mutant accumulating less than 5% of wild-type amts. was  
isolated after x-ray mutagenesis of C. reinhardtii cells. The recessive  
st-1-1 defect segregated as a single Mendelian mutation through meiosis,  
and led to a severe decrease in starch accumulation under all culture  
conditions tested, whether in the light or in darkness. Adenosine  
5'-diphosphoglucose pyrophosphorylase (in the absence of  
3-phosphoglycerate), starch synthase, phosphoglucomutase, phosphorylase,  
and starch-branching enzyme were all characterized and  
shown to be unaffected by the mutation. However, ADP-glucose  
pyrophosphorylase in the mutant had its sensitivity to activation by  
3-phosphoglycerate lowered dramatically and became less responsive to  
orthophosphate. The results are consistent both with a mutation in a  
structural gene of a multisubunit enzyme or in a regulatory gene  
responsible for switching ADP-glucose pyrophosphorylase from a  
3-phosphoglycerate-insensitive to a 3-phosphoglycerate-sensitive form.  
These results provide definite proof of the in vivo requirement for  
3-phosphoglycerate activation to obtain substantial starch synthesis in  
plants. The conclusions hold both for synthesis from CO<sub>2</sub> in the light or  
from exogenous organic C sources in darkness. A model is presented in which  
the existence of a 3-phosphoglycerate gradient explains localized starch  
synthesis around the pyrenoid of lower plants.

AN     1991:603057   HCAPLUS <<LOGINID::20100610>>

DN     115:203057

OREF   115:34553a,34556a

TI     A Chlamydomonas reinhardtii low-starch mutant is defective for  
3-phosphoglycerate activation and orthophosphate inhibition of ADP-glucose  
pyrophosphorylase

AU     Ball, Steven; Marianne, Therese; Dirick, Leon; Fresnoy, Marc; Delrue,  
Brigitte; Decq, Andre

CS     Lab. Chim. Biol., Univ. Sci. Tech. Lille Flandres-Artois, Villeneuve  
d'Ascq, F-59655, Fr.

SO     Planta (1991), 185(1), 17-26  
CODEN: PLANAB; ISSN: 0032-0935

DT     Journal

LA     English

OSC.G 51        THERE ARE 51 CAPLUS RECORDS THAT CITE THIS RECORD (51 CITINGS)

L3     ANSWER 16 OF 22   HCAPLUS   COPYRIGHT 2010 ACS on STN

TI     Polyglucan branching isoenzymes of algae

AB     The isoenzyme nature of the branching enzymes involved in the formation of  
the storage polyglucans of 3 algal species was investigated by  
using the method of Hedrick and Smith (CA 69:41618a) to analyze the  
results of polyacrylamide gel electrophoresis mobility studies. The red  
alga, Rhodomenia pertusa, contains 2 enzymes which act only on amylose to  
form moderately branched amylopectin (Q enzymes), and 1 with dual activity  
acting on both amylose and amylopectin to form highly branched  
phytoglycogens. Both the cyanophyte, Oscillatoria princeps, and the  
unclassified alga, Cyanidium caldarium, contain 2 enzymes with dual  
activity of the latter type. Analyses of the mobilities indicated that  
all 7 are isoenzymes, differing only in elec. charge, and probably are  
related in an evolutionary sense. The results suggest that C. caldarium  
belongs with the cyanophytes, or is a transition form between the  
blueGreen and red algae.

AN     1971:84012   HCAPLUS <<LOGINID::20100610>>

DN 74:84012  
OREF 74:13599a,13602a  
TI Polyglucan branching isoenzymes of algae  
AU Fredrick, Jerome F.  
CS Res. Lab., Dodge Chem. Co., Bronx, NY, USA  
SO Physiologia Plantarum (1971), 24(1), 55-8  
CODEN: PHPLAI; ISSN: 0031-9317  
DT Journal  
LA English  
OSC.G 1 THERE ARE 1 CAPLUS RECORDS THAT CITE THIS RECORD (1 CITINGS)

L3 ANSWER 17 OF 22 HCAPLUS COPYRIGHT 2010 ACS on STN  
TI Evolution of polyglucoside-synthesizing isozymes in the algae  
AB A review with 30 refs.  
AN 1971:29083 HCAPLUS <<LOGINID::20100610>>  
DN 74:29083  
OREF 74:4683a,4688a  
TI Evolution of polyglucoside-synthesizing isozymes in the algae  
AU Fredrick, Jerome F.  
CS Res. Lab., Dodge Chem. Co., Bronx, NY, USA  
SO Annals of the New York Academy of Sciences (1970), 175(Article 2), 524-30  
CODEN: ANYAA9; ISSN: 0077-8923  
DT Journal; General Review  
LA English

L3 ANSWER 18 OF 22 HCAPLUS COPYRIGHT 2010 ACS on STN  
TI Biochemical evolution of glucosyl transferase isozymes in algae  
AB Purified phosphorylase preps. from Oscillatoria, Rhodymenia, and Spirogyra, upon polyacrylamide gel electrophoresis, had 5 protein densitometric peaks. The demarcations were less distinct in Rhodymenia. In Spirogyra, protein a4 diminished, while protein a2 appeared to combine with protein a3. Proteins a1 and a2 were phosphorylases, and were similar to the a and b phosphorylases of animal tissues. Traces of a1 appeared in Rhodymenia. Enzymes a3 and a4 were active on both uridine diphosphoglucose (I) and adenosine diphosphoglucose (II); they were present in purified phosphorylase preps. of all 3 algae. The combined a3 and a2 enzyme in Spirogyra acted on I and II and glucose 1-phosphate. Fraction a4 diminished simultaneously. Protein a5 appeared to be a branching enzyme; it caused branching in amylose. Protein a5 was present in all 3 algae. ADP and UDP were released from nucleotide-glucose complexes.

AN 1968:493709 HCAPLUS <<LOGINID::20100610>>  
DN 69:93709  
OREF 69:17515a,17518a  
TI Biochemical evolution of glucosyl transferase isozymes in algae  
AU Fredrick, Jerome F.  
CS Div. of New York Res. Lab., Dodge Chem. Co., Bronx, NY, USA  
SO Annals of the New York Academy of Sciences (1968), 151(1), 413-23  
CODEN: ANYAA9; ISSN: 0077-8923  
DT Journal  
LA English  
OSC.G 1 THERE ARE 1 CAPLUS RECORDS THAT CITE THIS RECORD (1 CITINGS)

L3 ANSWER 19 OF 22 HCAPLUS COPYRIGHT 2010 ACS on STN  
TI Multiple forms of polyglucoside-branching enzyme in the algae  
AB Three isozymes specifically concerned with the branching of linear polyglucoside were detected in blue-green, red, and green algae, by using two-dimensional polyacrylamide-gel electrophoresis. Two isozymes were found in Oscillatoria princeps, three were present in Spirogyra setiformis, and two in red algae of the Rhodymenia species. The

degree of branching of the storage carbohydrate may be related to the evolutionary status of these algae.

AN 1968:102547 HCAPLUS <<LOGINID::20100610>>

DN 68:102547

OREF 68:19787a,19790a

TI Multiple forms of polyglucoside-branching enzyme in the algae

AU Fredrick, Jerome F.

CS Res. Lab., Dodge Chem. Co., Bronx, NY, USA

SO Physiologia Plantarum (1968), 21(1), 176-82

CODEN: PHPLAI; ISSN: 0031-9317

DT Journal

LA English

L3 ANSWER 20 OF 22 HCAPLUS COPYRIGHT 2010 ACS on STN

TI Effect of surface activity and chelation phenomena on the activity of the polyglucoside-synthesizing enzymes of Oscillatoria

AB A study was made of the effects of chelation and surface activity on the phosphorylase and the branching enzyme of the alga *Oscillatoria princeps*, as exhibited by the presence of both types of agents in the reaction mixts. (dipotassium salt of glucose-1-phosphate, 0.05M, NaHCO<sub>3</sub> buffer, and primer mols. of 0.1% amylose), as well as of the influence of a cationic surfactant combining both chelation and surface activity within its mols. The materials and procedures used are described and the results obtained are tabulated, plotted, and discussed. The ionic surfactants greatly inhibited the phosphorylase and branching enzyme of *Oscillatoria princeps*. The cationic surfactant inhibited the phosphorylase to a larger extent than the branching enzyme. The polyglucosides synthesized by mixts. of phosphorylase and branching enzymes ranged from normal to mutant types depending on which enzyme was more inhibited. It was concluded that the activity of the branching enzyme was the deciding factor of the type of sugar synthesized by mixts. of the two enzymes. A mechanism was suggested whereby the ionic surfactants were first attracted to the active centers of the enzyme by the specific charges on the enzyme mols.; the micelle formation and physical blocking of these centers prevented the enzyme-substrate union. The chelation phenomena, with regard to enzyme activity, was found to be mainly a detoxifying action whereby the toxic metallic ions were disrupted from their union with the enzyme proteins and rendered inert by chelation, thus restoring full activity to the enzyme mols. 37 references.

AN 1958:113993 HCAPLUS <<LOGINID::20100610>>

DN 52:113993

OREF 52:20279h-i,20280a-c

TI Effect of surface activity and chelation phenomena on the activity of the polyglucoside-synthesizing enzymes of Oscillatoria

AU Fredrick, Jerome F.

CS Dodge Chem. Co., New York, NY

SO Physiologia Plantarum (1957), 10, 844-57

CODEN: PHPLAI; ISSN: 0031-9317

DT Journal

LA English

L3 ANSWER 21 OF 22 HCAPLUS COPYRIGHT 2010 ACS on STN

TI The synthesis of polysaccharides in algae. V. Kinetics of polysaccharide formation in extracts of *Oscillatoria princeps*

AB cf. C.A. 47, 7609a. The application of reaction kinetics to the mixture of phosphorylase and branching enzyme in exts. from *O. princeps* must take into consideration the simultaneous action of both enzymes. The K<sub>s</sub> of branching enzyme is about 20 times that of phosphorylase. The kinetic analysis of polyglucoside production

by the interaction of these 2 enzymes on glucose-1-phosphate becomes quite complex and gives only an approximation.

AN 1955:69693 HCAPLUS <<LOGINID::20100610>>

DN 49:69693

OREF 49:13377f-g

TI The synthesis of polysaccharides in algae. V. Kinetics of polysaccharide formation in extracts of *Oscillatoria princeps*

AU Frederick, Jerome F.

CS Treasury Dept. Lab., New York, NY

SO *Physiologia Plantarum* (1954), 7, 182-9

CODEN: PHPLAI; ISSN: 0031-9317

DT Journal

LA Unavailable

L3 ANSWER 22 OF 22 HCAPLUS COPYRIGHT 2010 ACS on STN

TI Synthesis of polysaccharides in the algae. III. Induction of polysaccharide variants in *Oscillatoria princeps* by low temperatures

AB The usual polysaccharide synthesized by *O. princeps* is highly branched like glycogen, but the culture of single strands at 5-10° gives rise to variants which have a different cytological structure and synthesize only an unbranched polysaccharide. Enzyme preps. from these variants convert hexose phosphate to a straight-chain polysaccharide similar to amylose. Upon returning to 25-32° the low-temperature variants revert to a normal pattern of polysaccharide formation, but this treatment is without effect on the low-temperature enzyme exts. It is suggested

that a gene controlling the synthesis of a branching enzyme is altered at 5° and reverts to normal at 25°.

AN 1953:45044 HCAPLUS <<LOGINID::20100610>>

DN 47:45044

OREF 47:7608i,7609a-b

TI Synthesis of polysaccharides in the algae. III. Induction of polysaccharide variants in *Oscillatoria princeps* by low temperatures

AU Frederick, Jerome F.

CS New York Univ., New York, NY

SO *Physiologia Plantarum* (1953), 6, 96-9

CODEN: PHPLAI; ISSN: 0031-9317

DT Journal

LA Unavailable

=> file hcaplus

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FILE LAST UPDATED: 9 Jun 2010 (20100609/ED)  
REVISED CLASS FIELDS (/NCL) LAST RELOADED: Apr 2010  
USPTO MANUAL OF CLASSIFICATIONS THESAURUS ISSUE DATE: Apr 2010

HCAplus now includes complete International Patent Classification (IPC) reclassification data for the second quarter of 2010.

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This file contains CAS Registry Numbers for easy and accurate substance identification.

```
=> s branching enzyme
      65463 BRANCHING
      937081 ENZYME
L1      1369 BRANCHING ENZYME
          (BRANCHING(W)ENZYME)
```

```
=> s maize
L2      44820 MAIZE
```

```
=> s l1 and l2
L3      263 L1 AND L2
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```
=> s l3 and (PY<2000 or AY<2000 or PRY<2000)
      20131408 PY<2000
      3717474 AY<2000
      3181945 PRY<2000
L4      96 L3 AND (PY<2000 OR AY<2000 OR PRY<2000)
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MISSING OPERATOR ENZYME) 4A
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nested terms that are not separated by a logical operator.
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=> s (branching enzyme) (4a starch
MISSING OPERATOR ENZYME) (4A
The search profile that was entered contains terms or
nested terms that are not separated by a logical operator.
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      65463 BRANCHING
      937081 ENZYME
      1369 BRANCHING ENZYME
          (BRANCHING(W)ENZYME)
      202835 STARCH
L5      808 (BRANCHING ENZYME) (4A) (STARCH)
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      65463 BRANCHING
      937081 ENZYME
      1369 BRANCHING ENZYME
          (BRANCHING(W)ENZYME)
      202835 STARCH
      14914 AMYLOSE
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8082 AMYLOPECTIN  
L6 851 (BRANCHING ENZYME) (4A) (STARCH OR AMYLOSE OR AMYLOPECTIN)

=> s 12 and 16

L7 231 L2 AND L6

=> s 17 and (PY<2000 or AY<2000 or PRY<2000)

20131408 PY<2000

3717474 AY<2000

3181945 PRY<2000

L8 71 L7 AND (PY<2000 OR AY<2000 OR PRY<2000)

=> d 18 1-71 ti abs bib

L8 ANSWER 1 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN

TI Protein and cDNA sequences of corn gene dull1 coding for a starch synthase and use

AB The maize gene dull1 (dul) of the present invention is a determinant of the structure of endosperm starch. Mutations of dul affect the activity of at least two enzymes involved in starch biosynthesis, namely the starch synthase, SSII, and the starch branching enzyme, SBEIIa. Dul codes for a predicted 1674 residue protein, and is expressed with a unique temporal pattern in endosperm but is undetectable in leaf or root. The size of the Dul product and its expression pattern match precisely the known characteristics of maize SSII. The Dul product contains two different repeated regions in its unique amino terminus, one of which is identical to a conserved segment of the starch debranching enzymes. The cDNA provided for in the present invention encodes SSII, and mutations within this gene affect multiple aspects of starch biogenesis by disrupting an enzyme complex containing starch synthase(s), starch branching enzyme(s), and possibly starch debranching enzyme.

AN 2003:851297 HCAPLUS <<LOGINID::20100610>>

DN 139:334824

TI Protein and cDNA sequences of corn gene dull1 coding for a starch synthase and use

IN Myers, Alan M.; James, Martha Graham

PA Iowa State University Research Foundation, Inc., USA

SO U.S., 56 pp., Cont.-in-part of U.S. Ser. No. 968,542.

CODEN: USXXAM

DT Patent

LA English

FAN.CNT 2

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
	-----	----	-----	-----	-----
PI	US 6639125	B1	20031028	US 2000-554467	20000512 <--
	US 5981728	A	19991109	US 1997-968542	19971112 <--
	WO 9924575	A1	19990520	WO 1998-US24225	19981112 <--
	W:			AL, AM, AT, AU, AZ, BB, BG, BR, BY, CA, CH, CN, CZ, DE, DK, EE, ES, FI, GB, GE, HU, IL, IS, JP, KE, KG, KP, KR, KZ, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, TJ, TM, TR, TT, UA, UG, US, UZ, VN	
	RW:			GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG	
	US 20040049810	A1	20040311	US 2003-634262	20030805 <--
PRAI	US 1997-968542	A2	19971112	<--	
	WO 1998-US24225	W	19981112	<--	
	US 2000-554467	A1	20000512		

ASSIGNMENT HISTORY FOR US PATENT AVAILABLE IN LSUS DISPLAY FORMAT

OSC.G 1 THERE ARE 1 CAPLUS RECORDS THAT CITE THIS RECORD (1 CITINGS)  
RE.CNT 16 THERE ARE 16 CITED REFERENCES AVAILABLE FOR THIS RECORD  
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 2 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN  
TI The rice actin 2 promoter and intron and their use for plant transformation  
AB The current invention provides regulatory regions from the rice actin 2 gene. In particular, the current invention provides the rice actin 2 promoter and actin 2 intron. Compns. comprising these sequences are described, as well as transformation constructs derived therefrom. Further provided are methods for the expression of transgenes in plants comprising the use of these sequences. The methods of the invention include the direct creation of transgenic plants with the rice actin 2 intron and/or promoter directly by genetic transformation, as well as by plant breeding methods. The actin 2 sequences of the invention represent a valuable new tool for the creation of transgenic plants, preferably having one or more added beneficial characteristics.  
AN 2000:824429 HCAPLUS <<LOGINID::20100610>>  
DN 133:359795  
TI The rice actin 2 promoter and intron and their use for plant transformation  
IN McElroy, David; Wu, Ray  
PA Dekalb Genetics Corporation, USA; Cornell Research Foundation, Inc.  
SO PCT Int. Appl., 180 pp.  
CODEN: PIXXD2  
DT Patent  
LA English  
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2000070067	A1	20001123	WO 2000-US13303	20000512 <--
	W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW				
	RW: GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
	US 6429357	B1	20020806	US 1999-312304	19990514 <--
	CA 2372859	A1	20001123	CA 2000-2372859	20000512 <--
	EP 1179081	A1	20020213	EP 2000-942636	20000512 <--
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO				
	EP 2123764	A1	20091125	EP 2009-169512	20000512 <--
	R: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LI, LU, MC, NL, PT, SE				
PRAI	US 1999-312304	A1	19990514	<--	
	EP 2000-942636	A3	20000512		
	WO 2000-US13303	W	20000512		

ASSIGNMENT HISTORY FOR US PATENT AVAILABLE IN LSUS DISPLAY FORMAT  
OSC.G 3 THERE ARE 3 CAPLUS RECORDS THAT CITE THIS RECORD (3 CITINGS)  
RE.CNT 8 THERE ARE 8 CITED REFERENCES AVAILABLE FOR THIS RECORD  
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 3 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN  
TI Branched glucose soluble polymers and method for the production thereof  
AB The invention relates to glucose soluble polymers which do not substantially contain any  $\beta$ -glucosidic bonds, characterized in that they comprise 2.5-10%  $\alpha$ -1,6 glucosidic bonds, have a very low or zero tendency to

retrograde in an aqueous solution determined according to a test A, possess an  
MP which is determined according to a test C having a median value of the  
distribution profile of the mol. masses ranging from 104 and 105 Daltons  
and have a reducing sugar content that is at most 9%. The polymers could  
prepared from waxy maize starch by heating and degrading with  
enzyme.

AN 2000:790550 HCAPLUS <<LOGINID::20100610>>

DN 133:351718

TI Branched glucose soluble polymers and method for the production thereof

IN Caboche, Jean-jacques; Looten, Philippe; Petitjean, Carole; Fleche, Guy;  
Comini, Serge; Backer, Daniel

PA Roquette Freres, Fr.

SO PCT Int. Appl., 33 pp.

CODEN: PIXXD2

DT Patent

LA French

FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
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PI	WO 2000066633	A1	20001109	WO 2000-FR1109	20000426 <--
	W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR,				
	CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU,				
	ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU,				
	LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE,				
	SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW				
	RW: GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE,				
	DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF,				
	CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
	FR 2792941	A1	20001103	FR 1999-5523	19990430 <--
	FR 2792941	B1	20010727		
	CA 2371185	A1	20001109	CA 2000-2371185	20000426 <--
	EP 1177216	A1	20020206	EP 2000-922758	20000426 <--
	EP 1177216	B1	20040825		
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT,				
	IE, SI, LT, LV, FI, RO				
	JP 2002543248	T	20021217	JP 2000-615661	20000426 <--
	AT 274525	T	20040915	AT 2000-922758	20000426 <--
	AU 777378	B2	20041014	AU 2000-43052	20000426 <--
	PT 1177216	E	20050131	PT 2000-922758	20000426 <--
	ES 2226821	T3	20050401	ES 2000-922758	20000426 <--
	CN 1197878	C	20050420	CN 2000-806938	20000426 <--
	NO 2001005224	A	20011025	NO 2001-5224	20011025 <--
	MX 2001011078	A	20020722	MX 2001-11078	20011030 <--
	KR 803833	B1	20080214	KR 2001-713894	20011030 <--
PRAI	FR 1999-5523	A	19990430	<--	
	WO 2000-FR1109	W	20000426		

OSC.G 10 THERE ARE 10 CAPLUS RECORDS THAT CITE THIS RECORD (14 CITINGS)

RE.CNT 3 THERE ARE 3 CITED REFERENCES AVAILABLE FOR THIS RECORD

ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 4 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN

TI Biosynthesis of altered starch in genetically modified plants with  
glycogen branching enzyme gene

AB A method and compns. for altering starch properties in wheat and  
maize plants, starch obtained by such method, and transgenic  
plants producing such starch, are disclosed. Starch with altered  
properties is produced by introducing a gene construct comprising a  
glycogen branching enzyme coding sequence under the control of a promoter  
directing expression and a terminator. A transit peptide for  
translocation of the glycogen branching enzyme to the plant plastid may

also be included in the chimeric gene construct. The starch has altered processing characteristics, in particular an decreased chain length. A chimeric gene containing the High Mol. Weight Glutenin (HMWG) promoter, nopaline synthase terminator, and the transit-peptide region of the small-subunit of the ribulose biphosphate carboxylase (ssu of Rubisco) gene was utilized to direct expression of Escherichia coli glycogen branching enzyme (glgB) to wheat and maize. Expression of the glgB gene product in wheat and maize grain was detected by immunoblot anal. Anal. of the starch from these transgenic wheat and maize lines indicated an decrease in chain length, particularly an increase in chain length between 5 and 8 glucose units. The above parameters indicate a novel wheat and maize starch based on expression of the glgB E. coli gene product in transgenic plants.

AN 2000:368616 HCAPLUS <<LOGINID::20100610>>  
 DN 133:29689  
 TI Biosynthesis of altered starch in genetically modified plants with glycogen branching enzyme gene  
 IN Burrell, Michael Meyrick  
 PA Advanced Technologies (Cambridge) Limited, UK  
 SO PCT Int. Appl., 56 pp.  
 CODEN: PIXXD2  
 DT Patent  
 LA English  
 FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2000031282	A1	20000602	WO 1999-GB3762	19991108 <--
	W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, EE, ES, FI, GB, GE, GH, GM, HR, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, UZ, VN, YU, ZA, ZW				
	RW: GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
PRAI GB	1998-25262	A	19981119	<--	
OSC.G	1				THERE ARE 1 CAPLUS RECORDS THAT CITE THIS RECORD (1 CITINGS)
RE.CNT	8				THERE ARE 8 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 5 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN  
 TI Biosynthesis of altered starch in genetically modified plants with glycogen synthase gene  
 AB A method and compns. for altering starch properties in wheat and maize plants , starch obtained by such method, and transgenic plants producing such starch, are disclosed. Starch with altered properties is produced by introducing a gene construct comprising a glycogen synthase coding sequence under the control of a promoter directing expression and a terminator. A transit peptide for translocation of the glycogen synthase to the plant plastid may also be included in the chimeric gene construct. The starch has altered processing characteristics, in particular an increased chain length. A chimeric gene containing the High Mol. Weight Glutenin (HMWG) promoter, nopaline synthase terminator, and the transit-peptide region of the small-subunit of the ribulose biphosphate carboxylase (ssu of Rubisco) gene was utilized to direct expression of Escherichia coli glycogen synthase (glgA) to wheat and maize. Expression of the glgA gene product in wheat and maize grain was detected by immunoblot anal. Anal. of the starch from these transgenic wheat and maize lines indicated

an increase in chain length, particularly in chain length between 17 and 28 glucose units. Rapid viscometric anal. yielded lower peak and final viscosity values (about 30% of control values), whereas differential scanning calorimetry values indicated increased enthalpy values. The above parameters indicate a novel wheat and maize starch based on expression of the glgA E. coli gene product in transgenic plants.

AN 2000:368603 HCAPLUS <<LOGINID::20100610>>  
 DN 133:29688  
 TI Biosynthesis of altered starch in genetically modified plants with glycogen synthase gene  
 IN Burrell, Michael Meyrick  
 PA Advanced Technologies (Cambridge) Limited, UK  
 SO PCT Int. Appl., 66 pp.  
 CODEN: PIXXD2  
 DT Patent  
 LA English  
 FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2000031274	A1	20000602	WO 1999-GB3734	19991109 <--
	W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, EE, ES, FI, GB, GE, GH, GM, HR, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, UZ, VN, YU, ZA, ZW				
	RW: GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
	CA 2349819	A1	20000602	CA 1999-2349819	19991109 <--
	CA 2349819	C	20080909		
	EP 1131442	A1	20010912	EP 1999-954197	19991109 <--
	EP 1131442	B1	20100526		
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, CY				
	US 6468799	B1	20021022	US 1999-444728	19991118 <--
	AU 2000010616	A	20000807	AU 2000-10616	20000119 <--
	AU 2004202150	A1	20040617	AU 2004-202150	20040519
	AU 2004202150	B2	20060713		
PRAI	GB 1998-25242	A	19981119	<--	
	WO 1999-GB3734	W	19991109	<--	
	AU 2000-10616	A3	20000119		

ASSIGNMENT HISTORY FOR US PATENT AVAILABLE IN LSUS DISPLAY FORMAT

OSC.G 2 THERE ARE 2 CAPLUS RECORDS THAT CITE THIS RECORD (2 CITINGS)

RE.CNT 7 THERE ARE 7 CITED REFERENCES AVAILABLE FOR THIS RECORD

ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 6 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN

TI Starch branching enzyme II (SBEII-1 and SBEII-2) isoforms from wheat, cDNA, transgenic plants, and altering starch properties for food use

AB A class of wheat SBEII genes, SBEII-1, recombinant protein expression in transgenic plants, and its use in altering properties of starch produced by a plant are claimed. Starch properties include the gelatinization onset and/or peak temperature The use of such starch with altered properties in

food stuff, particularly bakery products is also claimed. CDNA clones for SBEII were isolated and sequenced. Those clones were divided into two sub-classes, SBEII-1 and SBEII-2 having sequence homol. to maize SBEIIb and SBEIIa, resp. These genes were mapped to the long arm of wheat group 2 homologous chromosomes. Some of those isoforms were expressed as recombinant protein in wheat. Differential scanning calorimetry studies

showed that starch produced in transgenic wheat transformed with expression construct for SBEII displayed higher onset, peak, and end temperature for gelatinization.

AN 2000:191230 HCAPLUS <<LOGINID::20100610>>

DN 132:247996

TI Starch branching enzyme II (SBEII-1 and SBEII-2) isoforms from wheat, cDNA, transgenic plants, and altering starch properties for food use

IN Goldsbrough, Andrew; Colliver, Steve

PA Plant Breeding International Cambridge Ltd., UK

SO PCT Int. Appl., 198 pp.

CODEN: PIXXD2

DT Patent

LA English

FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2000015810	A1	20000323	WO 1999-GB3011	19990909 <--
	W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZA, ZW				
	RW: GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
	AU 9958725	A	20000403	AU 1999-58725	19990909 <--
	AU 767103	B2	20031030		
	EP 1117814	A1	20010725	EP 1999-946307	19990909 <--
	EP 1117814	B1	20100217		
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, CY				
	HU 2001003618	A2	20020128	HU 2001-3618	19990909 <--
	HU 2001003618	A3	20031229		
	AT 458061	T	20100315	AT 1999-946307	19990909 <--
	US 6730825	B1	20040504	US 2001-786480	20010917 <--
	US 20040216188	A1	20041028	US 2004-818770	20040406 <--
	US 7217857	B2	20070515		
	US 20080064864	A1	20080313	US 2007-788837	20070419 <--
	US 7465851	B2	20081216		
PRAI	EP 1998-307337	A	19980910	<--	
	WO 1999-GB3011	W	19990909	<--	
	US 2001-786480	A3	20010917		
	US 2004-818770	A3	20040406		

ASSIGNMENT HISTORY FOR US PATENT AVAILABLE IN LSUS DISPLAY FORMAT

OSC.G 3 THERE ARE 3 CAPLUS RECORDS THAT CITE THIS RECORD (3 CITINGS)

RE.CNT 4 THERE ARE 4 CITED REFERENCES AVAILABLE FOR THIS RECORD

ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 7 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN

TI Modern biotechnology and maize starch biosynthesis

AB A review with 23 refs. The application of transgenic plants, gene cloning of biotechnol. in maize industry has been studied. This review extensive summarizes the research on the maize starch biosynthetic pathway consisted of substrate (ADP-GLC) formation, chain elongation, branch point insertion and trimming and the role of ADP-glucose pyrophosphorylase (AGP), starch synthetase (SS), starch branching enzyme (SBE) and identified starch debranching enzyme (DBE). The perspective on maize structure, function and biosynthetic pathway has also been made.

AN 1999:803454 HCAPLUS <<LOGINID::20100610>>  
 DN 132:323209  
 TI Modern biotechnology and maize starch biosynthesis  
 AU Qin, Jian; Su, Dongmin; Wang, Hongyan; Wang, Jinshui  
 CS Food Engineering Department, Zhengzhou Grain College, Zhengzhou, 450052,  
 Peop. Rep. China  
 SO Zhengzhou Liangshi Xueyuan Xuebao (1999), 20(3), 81-85, 88  
 CODEN: ZLXUEN; ISSN: 1000-2332  
 PB Zhengzhou Liangshi Xueyuan Xuebao Bianjibu  
 DT Journal; General Review  
 LA Chinese

L8 ANSWER 8 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN  
 TI Expression control elements from the 5'- and 3'-regions of genes for  
 starch branching enzymes  
 AB Regulatory elements from the 5'- and 3'-flanking regions of maize  
 genes for starch branching enzymes (SbeI and Ae) are described for use in  
 the expression of foreign genes in transgenic plants. The genes show  
 different patterns of expression in tissues of the seed during its  
 development and so the regulatory elements may be of use in the regulation  
 of foreign gene expression in cereals. The genes were cloned by screening  
 a genomic library with PCR products. The SbeI gene has a perfectly  
 palindromic G-box in the promoter region while the Ae gene had elements  
 resembling metal responsive elements, GC boxes, Hex, and I boxes.  
 Functional anal. of the SbeI promoter identified sequences responsible for  
 high level transcription and sugar regulation of gene expression. It also  
 showed that elements within the transcribed region play a role in high  
 level gene expression and that there sequences in the 5'-region that limit  
 gene expression. An essential region of 60 bp was identified and shown to  
 bind DNA-binding proteins.

AN 1999:795936 HCAPLUS <<LOGINID::20100610>>  
 DN 132:31802  
 TI Expression control elements from the 5'- and 3'-regions of genes for  
 starch branching enzymes  
 IN Guiltinan, Mark J.; Kim, Kyung-Nam  
 PA The Pennsylvania State University, USA  
 SO PCT Int. Appl., 110 pp.  
 CODEN: PIXXD2  
 DT Patent  
 LA English

FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 9964562	A2	19991216	WO 1999-US13266	19990611 <--
	WO 9964562	A3	20000518		
	W:	AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, UZ, VN, YU, ZA, ZW			
	RW:	GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG			
	AU 9944384	A	19991230	AU 1999-44384	19990611 <--
PRAI	US 1998-89049P	P	19980612	<--	
	US 1998-89050P	P	19980612	<--	
	WO 1999-US13266	W	19990611	<--	

RE.CNT 2 THERE ARE 2 CITED REFERENCES AVAILABLE FOR THIS RECORD  
 ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 9 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN



TI Carbon isotope ratios of amylose, amylopectin and mutant starches  
AB Carbon isotope ratios (expressed as  $\delta^{13}\text{C}$  values) were determined for various sources of starch and the starch fractions amylose and amylopectin. The  $\delta^{13}\text{C}$  values of amylose were consistently less neg., 0.4-2.3.permill., than those of amylopectin in kernel starch from maize (*Zea mays*) and barley (*Hordeum vulgare*) and in tuber starch from potato (*Solanum tuberosum*). Kernel starch isolated from the maize mutants wx1 and ael, with known genetic lesions in the starch biosynthetic pathway, also showed significant differences in  $\delta^{13}\text{C}$  values. Collectively, these results suggest that variation in carbon isotope ratios in the amylose and amylopectin components of starch may be attributed to isotopic discrimination by the enzymes involved in starch biosynthesis.

AN 1999:737017 HCAPLUS <<LOGINID::20100610>>  
DN 132:76065

TI Carbon isotope ratios of amylose, amylopectin and mutant starches  
AU Scott, M. Paul; Jane, Jay-Lin; Soundararajan, Madhavan  
CS USDA-ARS, Department of Agronomy, Iowa State University, Ames, IA, 50011, USA

SO Phytochemistry (1999), 52(4), 555-559  
CODEN: PYTCAS; ISSN: 0031-9422

PB Elsevier Science Ltd.

DT Journal

LA English

OSC.G 3 THERE ARE 3 CAPLUS RECORDS THAT CITE THIS RECORD (3 CITINGS)

RE.CNT 24 THERE ARE 24 CITED REFERENCES AVAILABLE FOR THIS RECORD  
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 10 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN

TI Expression of transgenes in plants using promoter and terminator sequences from Coix

AB Methods and compns. for the expression of transgenes in monocot plants including maize are disclosed. In the invention, gene silencing is avoided by use of monocot-homeologous sequences from plants of the genus Coix for transformation. Included in these transgene sequences are Coix promoters, enhancers, coding sequences and terminators. Suitable alternatives to maize-derived transgenes are desirable for expression in maize in that homol.-based gene silencing can limit or effectively eliminate transgene expression.

AN 1999:736897 HCAPLUS <<LOGINID::20100610>>  
DN 131:347500

TI Expression of transgenes in plants using promoter and terminator sequences from Coix

IN Kriz, Alan L.; Luethy, Michael H.; Voyles, Dale A.

PA Dekalb Genetics Corporation, USA

SO PCT Int. Appl., 240 pp.

CODEN: PIXXD2

DT Patent

LA English

FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
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PI	WO 9958659	A2	19991118	WO 1999-US10776	19990514 <--
	WO 9958659	A3	20000120		
	W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZA, ZW				
	RW: GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG,				

	CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG		
US 6635806	B1	20031021	US 1998-78972 19980514 <--
CA 2328129	A1	19991118	CA 1999-2328129 19990514 <--
AU 9939957	A	19991129	AU 1999-39957 19990514 <--
EP 1076706	A2	20010221	EP 1999-923112 19990514 <--
EP 1076706	B1	20080206	
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI, CY		
TR 2001000104	T2	20010621	TR 2001-104 19990514 <--
BR 9910455	A	20011127	BR 1999-10455 19990514 <--
JP 2002533057	T	20021008	JP 2000-548450 19990514 <--
AT 385518	T	20080215	AT 1999-923112 19990514 <--
PT 1076706	E	20080509	PT 1999-923112 19990514 <--
ES 2301239	T3	20080616	ES 1999-923112 19990514 <--
IN 2000DN00321	A	20080620	IN 2000-DN321 20001109 <--
IN 227562	A1	20090130	
ZA 2000006576	A	20020213	ZA 2000-6576 20001113 <--
MX 2000011199	A	20010419	MX 2000-11199 20001114 <--
US 20050250938	A1	20051110	US 2003-660097 20030911 <--
US 7256283	B2	20070814	
IN 2005DN05625	A	20070928	IN 2005-DN5625 20051205 <--
US 20080271212	A1	20081030	US 2007-838724 20070814 <--
US 20090013423	A1	20090108	US 2007-838725 20070814 <--
US 20090199307	A1	20090806	US 2007-838721 20070814 <--
PRAI US 1998-78972	A1	19980514	<--
WO 1999-US10776	W	19990514	<--
IN 2000-DN321	A3	20001109	
US 2003-660097	A3	20030911	

ASSIGNMENT HISTORY FOR US PATENT AVAILABLE IN LSUS DISPLAY FORMAT

OSC.G 5 THERE ARE 5 CAPLUS RECORDS THAT CITE THIS RECORD (8 CITINGS)

RE.CNT 1 THERE ARE 1 CITED REFERENCES AVAILABLE FOR THIS RECORD  
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 11 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN

TI Identification of cis-acting elements important for expression of the starch-branching enzyme I gene in maize endosperm

AB The genes encoding the starch-branching enzymes (SBE) SBEI, SBEIIa, and SBEIIb in maize (Zea mays) are differentially regulated in tissue specificity and during kernel development. To gain insight into the regulatory mechanisms controlling their expression, we analyzed the 5'-flanking sequences of Sbe1 using a transient gene expression system. Although the 2.2-kb 5'-flanking sequence between -2,190 and +27 relative to the transcription initiation site was sufficient to promote transcription, the addition of the transcribed region between +28 and +228 containing the first exon and intron resulted in high-level expression in suspension-cultured maize endosperm cells. A series of 5' deletion and linker-substitution mutants identified two critical pos. cis elements, -314 to -295 and -284 to -255. An electrophoretic mobility-shift assay showed that nuclear proteins prepared from maize kernels interact with the 60-bp fragment containing these two elements. Expression of the Sbe1 gene is regulated by sugar concentration in suspension-cultured maize endosperm cells, and the region -314 to -145 is essential for this effect. Interestingly, the expression of mEmBP-1, a bZIP transcription activator, in suspension-cultured maize endosperm cells resulted in a 5-fold decrease in Sbe1 promoter activity, suggesting a possible regulatory role of the G-box present in the Sbe1 promoter from -227 to -220.

AN 1999:615638 HCAPLUS <<LOGINID::20100610>>

DN 132:815

TI Identification of cis-acting elements important for expression of the

starch-branching enzyme I gene in  
maize endosperm

AU Kim, Kyung-Nam; Guiltinan, Mark J.

CS Intercollege Graduate Program in Plant Physiology, The Biotechnology  
Institute, and Department of Horticulture, The Pennsylvania State  
University, University Park, PA, 16802, USA

SO Plant Physiology (1999), 121(1), 225-236

CODEN: PLPHAY; ISSN: 0032-0889

PB American Society of Plant Physiologists

DT Journal

LA English

OSC.G 17 THERE ARE 17 CAPLUS RECORDS THAT CITE THIS RECORD (17 CITINGS)

RE.CNT 65 THERE ARE 65 CITED REFERENCES AVAILABLE FOR THIS RECORD

ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 12 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN

TI Maize starch synthase gene dul and uses in starch production

AB Disclosed are the maize dul gene, the encoded starch synthase  
isoenzyme II, and production of starch with recombinant dul-expressing cells  
or transgenic plants. The maize gene dull1 (dul) of the present  
invention is a determinant of the structure of endosperm starch.  
Mutations of dul affect the activity of at least two enzymes involved in  
starch biosynthesis, namely the starch synthase, SSII, and the  
starch branching enzyme, SBEIIa. Dul codes  
for a predicted 1674 residue protein, and is expressed with a unique  
temporal pattern in endosperm but is undetectable in leaf or root. The  
size of the Dul product and its expression pattern match precisely the  
known characteristics of maize SSII. The Dul product contains  
two different repeated regions in its unique amino terminus, one of which  
is identical to a conserved segment of the starch debranching enzymes.  
The cDNA provided for in the present invention encodes SSII, and mutations  
within this gene affect multiple aspects of starch biogenesis by  
disrupting an enzyme complex containing starch synthase(s),  
starch branching enzyme(s), and possibly  
starch debranching enzyme(s).

AN 1999:326050 HCAPLUS <<LOGINID::20100610>>

DN 130:333760

TI Maize starch synthase gene dul and uses in starch production

IN Myers, Alan M.; James, Martha G.

PA Iowa State University Research Foundation, Inc., USA

SO PCT Int. Appl., 138 pp.

CODEN: PIXXD2

DT Patent

LA English

FAN.CNT 2

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
	-----	---	-----	-----	-----
PI	WO 9924575	A1	19990520	WO 1998-US24225	19981112 <--
	W: AL, AM, AT, AU, AZ, BB, BG, BR, BY, CA, CH, CN, CZ, DE, DK, EE,				
	ES, FI, GB, GE, HU, IL, IS, JP, KE, KG, KP, KR, KZ, LK, LR, LS,				
	LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD,				
	SE, SG, SI, SK, TJ, TM, TR, TT, UA, UG, US, UZ, VN				
	RW: GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES,				
	FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI,				
	CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
	US 5981728	A	19991109	US 1997-968542	19971112 <--
	CA 2309346	A1	19990520	CA 1998-2309346	19981112 <--
	AU 9915236	A	19990531	AU 1999-15236	19981112 <--
	AU 761419	B2	20030605		
	EP 1030922	A1	20000830	EP 1998-959440	19981112 <--
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT,				

IE, FI

BR 9814864	A	20011106	BR 1998-14864	19981112 <--
JP 2001522604	T	20011120	JP 2000-520569	19981112 <--
NZ 504534	A	20021220	NZ 1998-504534	19981112 <--
MX 2000004586	A	20001110	MX 2000-4586	20000512 <--
US 6639125	B1	20031028	US 2000-554467	20000512 <--
PRAI US 1997-968542	A	19971112	<--	
WO 1998-US24225	W	19981112	<--	

ASSIGNMENT HISTORY FOR US PATENT AVAILABLE IN LSUS DISPLAY FORMAT

OSC.G 1 THERE ARE 1 CAPLUS RECORDS THAT CITE THIS RECORD (1 CITINGS)

RE.CNT 1 THERE ARE 1 CITED REFERENCES AVAILABLE FOR THIS RECORD

ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 13 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN

TI Characterization of a gene encoding wheat endosperm starch  
branching enzyme-I

AB A genomic DNA fragment from *Triticum tauschii*, the donor of the wheat D genome, contains a starch branching enzyme-I (SBE-I) gene spread over 6.5 kb. This gene (designated wSBE I-D4) encodes an amino acid sequence identical to that determined for the N-terminus of SBE-I from the hexaploid wheat (*T. aestivum*) endosperm. Cognate cDNA sequences for wSBE I-D4 were isolated from hexaploid wheat by hybridization screening from an endosperm library and also by PCR. A contiguous sequence (D4 cDNA) was assembled from the sequence of five overlapping partial cDNAs which spanned wSBE I-D4. D4 cDNA encodes a mature polypeptide of 87 kDa that shows 90% identity to SBE-I amino acid sequences from rice and maize and contains all the residues considered essential for activity. D4 mRNA has been detected only in the endosperm and is at a maximum concentration mid-way through grain development.

The

wSBE I-D4 gene consists of 14 exons, similar to the structure for the equivalent gene in rice; the rice gene has a strikingly longer intron 2. The 3' end of wSBE I-D4 was used to show that the gene is located on group 7 chromosomes. The sequence upstream of wSBE I-D4 was analyzed with respect to conserved motifs.

AN 1999:177589 HCAPLUS <<LOGINID::20100610>>

DN 131:83671

TI Characterization of a gene encoding wheat endosperm starch  
branching enzyme-I

AU Rahman, S.; Li, Z.; Abrahams, S.; Abbott, D.; Appels, R.; Morell, M. K.

CS CSIRO Plant Industry, Canberra, 2601, Australia

SO Theoretical and Applied Genetics (1999), 98(1), 156-163

CODEN: THAGA6; ISSN: 0040-5752

PB Springer-Verlag

DT Journal

LA English

OSC.G 24 THERE ARE 24 CAPLUS RECORDS THAT CITE THIS RECORD (24 CITINGS)

RE.CNT 32 THERE ARE 32 CITED REFERENCES AVAILABLE FOR THIS RECORD

ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 14 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN

TI Molecular cloning and characterization of the Amylose-Extender  
gene encoding starch branching enzyme IIB in  
maize

AB The amylose-extender (Ae) gene encoding starch-branching enzyme IIB (SBEIIB) in maize is predominantly expressed in endosperm and embryos during kernel development. A maize genomic DNA fragment (-2964 to +20485) containing the Ae gene was isolated and sequenced. The maize Ae mRNA is derived from 22 exons distributed over 16914 bp. Twenty-one introns, differing in length from 76 bp to 4020 bp, all have conserved junction sequences

(GT··AG). Sequence anal. of the 5'- and 3'-flanking regions revealed a consensus TATA-box sequence located 28 bp upstream of the transcription initiation site as determined by primer extension anal., and a putative polyadenylation signal observed 29 bp upstream of the polyadenylation site based on cDNA sequence. Genomic Southern blot anal. suggests that a single Ae gene is present in the maize genome. Promoter activity was confirmed by testing a transcriptional fusion of the Ae 5'-flanking region between -2964 and +100 to a luciferase reporter gene in a transient expression assay using maize endosperm suspension cultured cells. 5' deletion anal. revealed that the 111 bp region from -160 to -50 is essential for high-level promoter activity.

AN 1999:44300 HCAPLUS <<LOGINID::20100610>>

DN 130:219005

TI Molecular cloning and characterization of the Amylose-Extender gene encoding starch branching enzyme IIB in maize

AU Kim, Kyung-Nam; Fisher, Dane K.; Gao, Ming; Guiltinan, Mark J.

CS Intercollege Graduate Programs in Plant Physiology and Genetics, The Biotechnology Institute, and Department of Horticulture, The Pennsylvania State University, University Park, PA, 16802, USA

SO Plant Molecular Biology (1998), 38(6), 945-956

CODEN: PMBIDB; ISSN: 0167-4412

PB Kluwer Academic Publishers

DT Journal

LA English

OSC.G 26 THERE ARE 26 CAPLUS RECORDS THAT CITE THIS RECORD (26 CITINGS)

RE.CNT 55 THERE ARE 55 CITED REFERENCES AVAILABLE FOR THIS RECORD

ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 15 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN

TI Arginine residue 384 at the catalytic center is important for branching enzyme II from maize endosperm

AB Starch-branching enzyme (BE) belongs to the amylolytic family which contains 4 highly conserved regions. These regions are proposed to play an important role in catalysis as they are thought to be necessary for catalysis and/or binding the substrate. Only 1 Arg residue was found to be conserved in a catalytic center at the same position in all known sequences of BEs from various species as well as in the  $\alpha$ -amylase enzyme family. In maize BEII, a conserved Arg-384 residue is in catalytic region 2. Here, the authors used site-directed mutagenesis of Arg-384 in order to study its possible role in BE. Previous chemical modification studies suggested that it may play a role in substrate binding. Replacement of Arg-384 by Ala, Ser, Gln, and Glu in the active site caused almost total inactivation. However, a conservative mutation of the conserved Arg-384 residue by Lys resulted in some residual activity, .apprx.5% of that of the wild-type enzyme. The reaction kinetics of the purified mutant R384K enzyme were investigated and no large effect on the Km of the substrate, amylose, for BEII was observed. Thus, these results suggest that conserved Arg-384 in maize BEII plays an important role in the catalytic function of BEs but may not be directly involved in substrate binding. (c) 1998 Academic Press.

AN 1998:797799 HCAPLUS <<LOGINID::20100610>>

DN 130:121370

TI Arginine residue 384 at the catalytic center is important for branching enzyme II from maize endosperm

AU Libessart, Nathalie; Preiss, Jack

CS Department of Biochemistry, Michigan State University, East Lansing, MI, 48824, USA

SO Archives of Biochemistry and Biophysics (1998), 360(1), 135-141

CODEN: ABBIA4; ISSN: 0003-9861

PB Academic Press

DT Journal  
LA English  
OSC.G 13 THERE ARE 13 CAPLUS RECORDS THAT CITE THIS RECORD (13 CITINGS)  
RE.CNT 56 THERE ARE 56 CITED REFERENCES AVAILABLE FOR THIS RECORD  
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 16 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN  
TI Manipulating the starch composition of potato  
AB A review with 41 refs. Starch can be fractionated into two types of glucose polymers: amylose and amylopectin. Amylose consists of essentially linear chains of  $\alpha$ -(1,4)-linked glucose residues, whereas amylopectin is built up from  $\alpha$ -(1,4)-linked chains with  $\alpha$ -(1,6)-linked branches. The composition and fine structure of starch are responsible for many of the physicochem. properties and thus det. its industrial uses. Variation in starch structure and composition can be found between and within crops. In the latter case it can be found in mutants, often resulting from the loss of function of one or more of the genes involved in starch biosynthesis. In maize, the most extensively studied crop, mutant genotypes are known for nearly every gene identified as being involved in starch biosynthesis. Differences in starch composition can also be achieved by genetic modifications such as antisense inhibition of genes or overexpression of (heterologous) genes. Most examples of genetic modification of starch composition are in potato, which can easily be transformed. Antisense inhibition of enzymes in the biosynthetic pathway, such as ADP glucose phosphorylase (AGP), (granule-bound) starch synthase or branching enzyme, lead to an altered starch content and/or composition. In addition, the introduction and expression of bacterial genes, such as genes of the Escherichia coli glycogen synthesis pathway, in potato leads to starches with altered content, composition, structure and physicochem. properties. Studying the physicochem. properties of these altered starches will, together with the information obtained by research on starches of mutants, help to clarify the precise relationship between structural and functional features of starch.

AN 1998:787972 HCAPLUS <<LOGINID::20100610>>  
DN 130:165463  
TI Manipulating the starch composition of potato  
AU Kortstee, A. J.; Flipse, E.; Kuipers, A. G. J.; Jacobsen, E.; Visser, R. G. F.  
CS Graduate School of Experimental Plant Sciences, Department of Plant Breeding, Agricultural University Wageningen, Wageningen, 6700 AJ, Neth.  
SO Portland Press Proceedings (1998), 14(Engineering Crop Plants for Industrial End Uses), 89-98  
CODEN: POPPEF; ISSN: 0966-4068  
PB Portland Press Ltd.  
DT Journal; General Review  
LA English  
OSC.G 1 THERE ARE 1 CAPLUS RECORDS THAT CITE THIS RECORD (1 CITINGS)  
RE.CNT 41 THERE ARE 41 CITED REFERENCES AVAILABLE FOR THIS RECORD  
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 17 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN  
TI Analysis of essential histidine residues of maize branching enzymes by chemical modification and site-directed mutagenesis  
AB Incubation of maize branching enzyme, mBEI and mBEII, with 100  $\mu$ M diethylpyrocarbonate (DEPC) rapidly inactivated the enzymes. Treatment of the DEPC-inactivated enzymes with 100-500 mM hydroxylamine restored the enzyme activities. Spectroscopic data indicated that the inactivation of BE with DEPC was the result of histidine modification. The addition of the substrate amylose or amylopectin retarded the enzyme inactivation by DEPC, suggesting that the histidine residues are important

for substrate binding. In maize BEII, conserved histidine residues are in catalytic regions 1 (His320) and 4 (His508). His320 and His508 were individually replaced by Ala via site-directed mutagenesis to probe their role in catalysis. Expression of these mutants in *E. coli* showed a significant decrease of the activity and the mutant enzymes had  $K_m$  values 10 times higher than the wild type. Therefore, residues His320 and His508 do play an important role in substrate binding.

AN 1998:784558 HCAPLUS <<LOGINID::20100610>>

DN 130:121357

TI Analysis of essential histidine residues of maize branching enzymes by chemical modification and site-directed mutagenesis

AU Funane, Kazumi; Libessart, Nathalie; Stewart, Douglas; Michishita, Toru; Preiss, Jack

CS Department of Biochemistry, Michigan State University, East Lansing, MI, 48824, USA

SO Journal of Protein Chemistry (1998), 17(7), 579-590

CODEN: JPCHD2; ISSN: 0277-8033

PB Plenum Publishing Corp.

DT Journal

LA English

OSC.G 10 THERE ARE 10 CAPLUS RECORDS THAT CITE THIS RECORD (10 CITINGS)

RE.CNT 54 THERE ARE 54 CITED REFERENCES AVAILABLE FOR THIS RECORD

ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 18 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN

TI Starch biosynthesis: understanding the functions and interactions of multiple isoenzymes of starch synthase and branching enzyme

AB A review with 47 refs. Starch is the most important source of calories on the planet and a vital storage compound in plants. Despite its importance, we do not fully understand how starch is synthesized, how starch synthesis is initiated and what controls starch structure. Many genes in the starch biosynthesis pathway have been isolated and multiple forms of starch synthase and branching enzyme have been identified. For example, five starch synthase genes and three branching enzyme genes have been cloned from maize. To fully illustrate the mechanism of starch biosynthesis, we need to understand the functions of individual enzyme as well as the concerted actions of multiple forms of enzymes in starch synthesis. Since maize is the number one supply of starch for food and non-food industries and also a good source for genetic and biochem. studies, here we will use maize as a model plant to discuss the mechanism of starch biosynthesis, particularly the initiation of starch synthesis, the functions and interaction of multiple isoenzymes of starch synthase and branching enzyme.

AN 1998:643789 HCAPLUS <<LOGINID::20100610>>

DN 130:48960

TI Starch biosynthesis: understanding the functions and interactions of multiple isoenzymes of starch synthase and branching enzyme

AU Guan, H. P.; Keeling, P. L.

CS ExSeed Genetics L. L. C. and Agronomy Department, Iowa State University, Ames, IA, 50011, USA

SO Trends in Glycoscience and Glycotechnology (1998), 10(54), 307-319

CODEN: TGGLEE; ISSN: 0915-7352

PB FCCA

DT Journal; General Review

LA English

OSC.G 14 THERE ARE 14 CAPLUS RECORDS THAT CITE THIS RECORD (14 CITINGS)

RE.CNT 47 THERE ARE 47 CITED REFERENCES AVAILABLE FOR THIS RECORD

ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 19 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN  
 TI Genomic organization and promoter activity of the maize starch branching enzyme I gene  
 AB Starch branching enzymes (SBE) which catalyze the formation of  $\alpha$ -1,6-glucan linkages are of crucial importance for the quantity and quality of starch synthesized in plants. In maize (*Zea mays* L.), three SBE isoforms (SBEI, IIa and IIb) have been identified and shown to exhibit differential expression patterns. As a first step toward understanding the regulatory mechanisms controlling their expression, the authors isolated and sequenced a maize genomic DNA (-2190 to +5929) which contains the entire coding region of SBEI (Sbe1) as well as 5'-and 3'-flanking sequences. Using this clone, the authors established a complete genomic organization of the maize Sbe1 gene. The transcribed region consists of 14 exons and 13 introns, distributed over 5.7 kb. A consensus TATA-box and a G-box containing a perfect palindromic sequence, CCACGTGG, were found in the 5'-flanking region. Genomic Southern blot anal. indicated that two Sbe1 genes with divergent 5'-flanking sequences exist in the maize genome, suggesting the possibility that they are differentially regulated. A chimeric construct containing the 5'-flanking region of Sbe1 (-2190 to +27) fused to the  $\beta$ -glucuronidase gene (pKG101) showed promoter activity after it was introduced into maize endosperm suspension cells by particle bombardment.  
 AN 1998:597027 HCAPLUS <<LOGINID::20100610>>  
 DN 129:311547  
 OREF 129:63465a,63468a  
 TI Genomic organization and promoter activity of the maize starch branching enzyme I gene  
 AU Kim, Kyung-Nam; Fisher, Dane K.; Gao, Ming; Guiltinan, Mark J.  
 CS Intercollege Graduate Programs in Plant Physiology and Genetics, Biotechnology Institute, Dep. Horticulture, Pennsylvania State University, Pennsylvania, PA, 16802, USA  
 SO Gene (1998), 216(2), 233-243  
 CODEN: GENED6; ISSN: 0378-1119  
 PB Elsevier Science B.V.  
 DT Journal  
 LA English  
 OSC.G 13 THERE ARE 13 CAPLUS RECORDS THAT CITE THIS RECORD (13 CITINGS)  
 RE.CNT 42 THERE ARE 42 CITED REFERENCES AVAILABLE FOR THIS RECORD  
 ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 20 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN  
 TI Altering starch structure and functionality by manipulating expression of starch biosynthetic enzymes.  
 AB Starch functionality is a product of the fine structure of a given starch polymer. This structure is a result of the concerted action of several starch synthases, starch branching enzymes and starch debranching enzymes. To examine the relationship between starch polymer structure and starch functionality we are using transgenic approaches to control the expression of genes encoding starch biosynthetic enzymes and examine the impacts of altered gene expression on starch structure and functionality. We have isolated and characterized maize cDNAs encoding Starch Branching Enzymes I and IIb (SBE I SBEIIb) and generated transgenic maize plants carrying constructions for under and over expression of these two genes. The effects of altered branching enzyme expression on starch polymer structure and starch functionality will be presented.  
 AN 1998:530122 HCAPLUS <<LOGINID::20100610>>  
 TI Altering starch structure and functionality by manipulating expression of



starch biosynthetic enzymes.

AU Lightner, Jonathan; Broglie, Karen; Cressman, Robert; Hines, Chris;  
Pearlstein, Rich; Hubbard, Natalie

CS Stine-Haskell Research Center, DuPont Agricultural Products, Newark, DE,  
19714-0030, USA

SO Book of Abstracts, 216th ACS National Meeting, Boston, August 23-27 (  
1998), AGFD-137 Publisher: American Chemical Society, Washington,  
D. C.  
CODEN: 66KYA2

DT Conference; Meeting Abstract

LA English

L8 ANSWER 21 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN

TI Heat-induced fragmentation of the maize waxy protein during  
protein extraction from starch granules

AB The starch granule of maize contains a characteristic set of  
tightly bound polypeptides. Granule-associated polypeptides are typically  
extracted from starch granules by heating starch granule suspensions at  
90-100°C in a detergent such as SDS. Solubilized proteins are  
recovered by centrifugation and analyzed by gel electrophoresis.  
Previously identified tightly bound granule intrinsic proteins consist of  
the 85-kDa starch-branching enzyme IIb, the  
76-kDa starch synthase I, and the 60-kD waxy (Wx) protein, also  
known as granule-bound starch synthase I. However, SDS exts. from starch  
granules of maize also contain a cluster of proteins ranging in  
mass between 47 and 32 kDa In this study, we analyzed this group of  
granule-associated proteins and found that each was recognized by the Wx  
antibody. A 15 amino acid N-terminal sequence from the 47-kDa polypeptide  
was identical to the predicted N-terminus of the Wx protein. Further  
anal. revealed that each immunoreactive polypeptide between 47 and 32 kDa  
was a heat-induced fragmentation product of the Wx protein. Conditions  
for the extraction of granule proteins were evaluated. Our results demonstrate  
that granule proteins are effectively released by mild extraction (10-min  
incubation at 72°C). Relative to the Wx protein, starch  
synthase I and starch branching enzyme IIb  
were less susceptible to thermal fragmentation. These results demonstrate  
that the 85-, 76-, and 60-kDa polypeptides are authentic granule-intrinsic  
proteins, and that the majority of polypeptides between 47 and 32 kDa are  
artifacts of high-temperature granule extraction procedures.

AN 1998:485937 HCAPLUS <<LOGINID::20100610>>

DN 129:188502

OREF 129:38301a,38304a

TI Heat-induced fragmentation of the maize waxy protein during  
protein extraction from starch granules

AU Mu, Helen He; Mu-Forster, Chen; Bohonko, Monica; Wasserman, Bruce P.

CS Department of Food Science, New Jersey Agricultural Experiment Station,  
Cook College, Rutgers University, New Brunswick, NJ, HEAT-INDUCED FRAGMEN,  
USA

SO Cereal Chemistry (1998), 75(4), 480-483  
CODEN: CECHAF; ISSN: 0009-0352

PB American Association of Cereal Chemists

DT Journal

LA English

OSC.G 8 THERE ARE 8 CAPLUS RECORDS THAT CITE THIS RECORD (8 CITINGS)

RE.CNT 20 THERE ARE 20 CITED REFERENCES AVAILABLE FOR THIS RECORD  
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 22 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN

TI Starch granule-associated protein and transgenic plants producing starch  
with altered viscosity and phosphate content

AB Nucleic acid mols. are described encoding a starch granule-bound protein

from potato and maize as well as methods and recombinant DNA mols. for the production of transgenic plant cells and plants synthesizing a modified starch. Potato and maize cDNAs for a starch granule-associated protein were cloned and sequenced. Transgenic potatoes expressing an antisense version of the potato cDNA produced starch with .apprx.50% lower phosphate content and with altered gelling properties. When the starch granule-associated protein cDNA was expressed in Escherichia coli, glycogen with higher than normal phosphate content was produced.

AN 1998:424347 HCAPLUS <<LOGINID::20100610>>

DN 129:91420

OREF 129:18743a,18746a

TI Starch granule-associated protein and transgenic plants producing starch with altered viscosity and phosphate content

IN Kossmann, Jens; Emmermann, Michael

PA Planttec Biotechnologie G.m.b.H., Germany

SO PCT Int. Appl., 123 pp.

CODEN: PIXXD2

DT Patent

LA English

FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 9827212	A1	19980625	WO 1997-EP7123	19971218 <--
	W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, GW, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW				
	RW: GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG				
	DE 19653176	A1	19980625	DE 1996-19653176	19961219 <--
	CA 2272844	A1	19980625	CA 1997-2272844	19971218 <--
	AU 9858577	A	19980715	AU 1998-58577	19971218 <--
	AU 740492	B2	20011108		
	EP 950107	A1	19991020	EP 1997-954424	19971218 <--
	EP 950107	B1	20070321		
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, NL, SE, PT				
	JP 2001522223	T	20011113	JP 1998-527334	19971218 <--
	JP 4098365	B2	20080611		
	AT 357522	T	20070415	AT 1997-954424	19971218 <--
	PT 950107	E	20070531	PT 1997-954424	19971218 <--
	ES 2280086	T3	20070901	ES 1997-954424	19971218 <--
	US 7186898	B1	20070306	US 1999-334103	19990616 <--
PRAI	DE 1996-19653176	A	19961219	<--	
	WO 1997-EP7123	W	19971218	<--	

ASSIGNMENT HISTORY FOR US PATENT AVAILABLE IN LSUS DISPLAY FORMAT

OSC.G 9 THERE ARE 9 CAPLUS RECORDS THAT CITE THIS RECORD (9 CITINGS)

RE.CNT 4 THERE ARE 4 CITED REFERENCES AVAILABLE FOR THIS RECORD

ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 23 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN

TI Characterization of the difference of starch branching enzyme activities in normal and low-amylopectin maize during kernel development

AB In order to determine the reasons for the differences in structure between starch from a normal and a low-amylopectin maize variety, the activities of all the enzymes in the committed pathway of starch synthesis were studied throughout kernel development. Levels of ADP glucose pyrophosphorylase and starch synthase activity were found to be broadly similar between the two varieties but the low-amylopectin starch (LAPS)

maize variety showed dramatically reduced starch branching enzyme activity, with an almost total absence of the branching enzyme II isoform. SEM showed a significant alteration in the morphol. of the starch granules of the low-amylopectin maize. The results suggest that the increased amylose and the reduction of high mol. weight amylopectin in the LAPS starch results from the absence of the branching enzyme II isoform. This evidence suggests that the different branching enzyme isoforms contribute sep. to the synthesis and final structure of amylopectin.

AN 1998:418224 HCAPLUS <<LOGINID::20100610>>

DN 129:186465

OREF 129:37801a,37804a

TI Characterization of the difference of starch branching enzyme activities in normal and low-amylopectin maize during kernel development

AU Sidebottom, C.; Kirkland, M.; Strongitharm, B.; Jeffcoat, R.

CS Biosciences Division, Unilever Research, Bedford, MK44 1LQ, UK

SO Journal of Cereal Science (1998), 27(3), 279-287

CODEN: JCSCDA; ISSN: 0733-5210

PB Academic Press Ltd.

DT Journal

LA English

OSC.G 20 THERE ARE 20 CAPLUS RECORDS THAT CITE THIS RECORD (20 CITINGS)

RE.CNT 22 THERE ARE 22 CITED REFERENCES AVAILABLE FOR THIS RECORD

ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 24 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN

TI Surface localization of zein storage proteins in starch granules from maize endosperm. Proteolytic removal by thermolysin and in vitro crosslinking of granule-associated polypeptides

AB Starch granules from maize (*Zea mays*) contain a characteristic group of polypeptides that are tightly associated with the starch matrix (C. Mu-Forster, et al ,1996). Zeins comprise about 50% of the granule-associated proteins, and their spatial distribution within the starch granule was determined. Proteolysis of starch granules at subgelatinization temps. using the thermophilic protease thermolysin led to selective removal of the zeins, whereas granule-associated proteins of 32 kD or above, including the waxy protein, starch synthase I, and starch-branching enzyme 11b, remained refractory to proteolysis. Granule-associated proteins from maize are therefore composed of two distinct classes, the surface-localized zeins of 10 to 27 kD and the granule-intrinsic proteins of 32 kD or higher. The origin of surface-localized  $\delta$ -zein was probed by comparing  $\delta$ -zein levels of starch granules obtained from homogenized whole endosperm with granules isolated from amyloplasts. Starch granules from amyloplasts contained markedly lower levels of  $\delta$ -zein relative to granules prepared from whole endosperm, thus indicating that  $\delta$ -zein adheres to granule surfaces after disruption of the amyloplast envelope. Crosslinking expts. show that the zeins are deposited on the granule surface as aggregates. In contrast, the granule-intrinsic proteins are prone to covalent modification, but do not form intermol. cross-links. Thus, individual granule intrinsic proteins exist as monomers and are not deposited in the form of multimeric clusters within the starch matrix.

AN 1998:258959 HCAPLUS <<LOGINID::20100610>>

DN 129:2723

OREF 129:667a,670a

TI Surface localization of zein storage proteins in starch granules from maize endosperm. Proteolytic removal by thermolysin and in vitro crosslinking of granule-associated polypeptides

AU Mu-Forster, Chen; Wasserman, Bruce P.

CS Department of Food Science Cook College, New Jersey Agricultural

Experiment Station, Rutgers University, New Brunswick, NJ, 08901-8520, USA  
SO Plant Physiology (1998), 116(4), 1563-1571  
CODEN: PLPHAY; ISSN: 0032-0889  
PB American Society of Plant Physiologists  
DT Journal  
LA English

OSC.G 26 THERE ARE 26 CAPLUS RECORDS THAT CITE THIS RECORD (26 CITINGS)  
RE.CNT 46 THERE ARE 46 CITED REFERENCES AVAILABLE FOR THIS RECORD  
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 25 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN  
TI Polypeptides of the maize amyloplast stroma. Stromal  
localization of starch-biosynthetic enzymes and identification of an  
81-kilodalton amyloplast stromal heat-shock cognate  
AB In the developing endosperm of monocotyledonous plants, starch granules  
are synthesized and deposited within the amyloplast. A soluble stromal  
fraction was isolated from amyloplasts of immature maize (Zea  
mays L.) endosperm and analyzed for enzyme activities and polypeptide  
content. Specific activities of starch synthase and  
starch-branching enzyme (SBE), but not the  
cytosolic marker alc. dehydrogenase, were strongly enhanced in soluble  
amyloplast stromal fractions relative to soluble exts. obtained from  
homogenized kernels or endosperms. Immunoblot anal. demonstrated that  
starch synthase 1, SBEIIb, and sugary1, the putative starch-debranching  
enzyme, were each highly enriched in the amyloplast stroma, providing  
direct evidence for the localization of starch-biosynthetic enzymes within  
this compartment. Anal. of maize mutants shows the deficiency  
of the 85-kD SBEIIb polypeptide in the stroma of amylose extender  
cultivars and that the dull mutant lacks a >220-kD stromal polypeptide.  
The stromal fraction is distinguished by differential enrichment of a  
characteristic group of previously undocumented polypeptides. N-terminal  
sequence anal. revealed that an abundant 81-kD stromal polypeptide is a  
member of the Hsp70 family of stress-related proteins. Moreover, the  
81-kD stromal polypeptide is strongly recognized by antibodies specific  
for an Hsp70 of the chloroplast stroma. These findings are discussed in  
light of implications for the correct folding and assembly of soluble,  
partially soluble, and granule-bound starch-biosynthetic enzymes during  
import into the amyloplast.

AN 1998:258947 HCAPLUS <<LOGINID::20100610>>

DN 129:2721

OREF 129:667a,670a

TI Polypeptides of the maize amyloplast stroma. Stromal  
localization of starch-biosynthetic enzymes and identification of an  
81-kilodalton amyloplast stromal heat-shock cognate

AU Yu, Ying; Mu, Helen He; Mu-Forster, Chen; Wasserman, Bruce P.

CS Department of Food Science Cook College, New Jersey Agricultural  
Experiment Station Rutgers University, New Brunswick, NJ, 08901-8520, USA

SO Plant Physiology (1998), 116(4), 1451-1460  
CODEN: PLPHAY; ISSN: 0032-0889

PB American Society of Plant Physiologists

DT Journal

LA English

OSC.G 19 THERE ARE 19 CAPLUS RECORDS THAT CITE THIS RECORD (19 CITINGS)  
RE.CNT 49 THERE ARE 49 CITED REFERENCES AVAILABLE FOR THIS RECORD  
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 26 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN  
TI Promoter of wheat wbeI gene for expressing foreign genes in  
monocotyledonous plants  
AB A DNA fragment for directing the expression of foreign or endogenous genes  
or RNA in cells of monocot plants. The fragment comprises a sequence

corresponding to a first part of a putative type I starch branching enzyme gene (wbeI) present in wheat and a 5'-region upstream of the gene, or a part of the sequence that is effective for increasing the expression of the foreign or endogenous gene in the plant cells. The indicated sequence contains two promoter regions, P1 and P2. A DNA fragment effective to increase expression comprises at least one of the promoter regions, or an effective part. The fragment can be obtained from a genomic library of wheat and can be fused to suitable genes and markers and inserted into suitable vectors for expression in transgenic monocot plants. The P2 promoter, found in the second intron, was 2-4 times more active in wheat, barley, oat and maize cells than the P1-P2 combination.

AN 1998:256690 HCAPLUS <<LOGINID::20100610>>

DN 128:253799

OREF 128:50155a,50158a

TI Promoter of wheat wbeI gene for expressing foreign genes in monocotyledonous plants

IN Baga, Monica; Chibbar, Ravindra N.; Kartha, Kutty K.

PA Baga, Monica, Can.; Chibbar, Ravindra N.; Kartha, Kutty K.

SO Can. Pat. Appl., 78 pp.

CODEN: CPXXEB

DT Patent

LA English

FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	CA 2196834	A1	19971204	CA 1997-2196834	19970205 <--
	US 5866793	A	19990202	US 1996-773251	19961223 <--
PRAI	CA 1996-2178016	A	19960603	<--	

ASSIGNMENT HISTORY FOR US PATENT AVAILABLE IN LSUS DISPLAY FORMAT

OSC.G 5 THERE ARE 5 CAPLUS RECORDS THAT CITE THIS RECORD (5 CITINGS)

L8 ANSWER 27 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN

TI Characterization of dull1, a maize gene coding for a novel starch synthase

AB The maize dull1 (dul) gene is a determinant of the structure of endosperm starch, and dul-mutations affect the activity of two enzymes involved in starch biosynthesis, starch synthase II (SSII) and starch branching enzyme IIa (SBEIIa). Six novel dul-mutations generated in Mutator-active plants were identified. A portion of the dul locus was cloned by transposon tagging, and a nearly full-length Dul cDNA sequence was determined. Dul codes for a predicted 1674-residue protein, comprising one portion that is similar to SSIII of potato, as well as a large unique region. Dul transcripts are present in the endosperm during the time of starch biosynthesis, but the mRNA was undetectable in leaf or root tissue. The predicted size of the Dul gene product and its expression pattern are consistent with those of maize SSII. The Dul gene product contains two repeated regions in its unique N terminus. One of these contains a sequence identical to a conserved segment of SBEs. We conclude that Dul codes for a starch synthase, most likely SSII, and that secondary effects of dul-mutations, such as reduction of SBEIIa, result from the primary deficiency in this starch synthase.

AN 1998:215485 HCAPLUS <<LOGINID::20100610>>

DN 129:2125

OREF 129:531a,534a

TI Characterization of dull1, a maize gene coding for a novel starch synthase

AU Gao, Ming; Wanat, Jennifer; Stinard, Philip S.; James, Martha G.; Myers, Alan M.

CS Department of Biochemistry and Biophysics, Iowa State University, Ames,

IA, 50011, USA

SO Plant Cell (1998), 10(3), 399-412  
CODEN: PLCEEW; ISSN: 1040-4651

PB American Society of Plant Physiologists

DT Journal

LA English

OSC.G 100 THERE ARE 100 CAPLUS RECORDS THAT CITE THIS RECORD (100 CITINGS)

RE.CNT 56 THERE ARE 56 CITED REFERENCES AVAILABLE FOR THIS RECORD  
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 28 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN

TI Linkage mapping of starch branching enzyme  
III in rice (*Oryza sativa* L.) and prediction of location of orthologous  
genes in other grasses

AB The chromosomal position of Starch Branching  
Enzyme III (SBEIII) was determined via linkage to RFLP markers on an  
existing mol. map of rice (*Oryza sativa* L.). A cDNA of 890 bp was  
generated using specific PCR primers designed from available SBEIII  
sequence data and used as a probe in Southern anal. The SBEIII cDNA  
hybridized to multiple restriction fragments, but these fragments mapped  
to a single locus on rice chromosome 2, flanked by CD0718 and RG157. The  
detection of a multiple-copy hybridization pattern suggested the  
possibility of a tandemly duplicated gene at this locus. The map location  
of orthologous SBE genes in maize, wheat, and oat were predicted  
based on previously published genetic studies and comparative maps of the  
grass family.

AN 1997:370751 HCAPLUS <<LOGINID::20100610>>

DN 127:14031

OREF 127:2763a,2766a

TI Linkage mapping of starch branching enzyme  
III in rice (*Oryza sativa* L.) and prediction of location of orthologous  
genes in other grasses

AU Harrington, S. E.; Bligh, H. F. J.; Park, W. D.; Jones, C. A.; McCouch, S.  
R.

CS Development Plant Breeding Biometry, Cornell University, Ithaca, NY,  
14853-1902, USA

SO Theoretical and Applied Genetics (1997), 94(5), 564-568  
CODEN: THAGA6; ISSN: 0040-5752

PB Springer

DT Journal

LA English

OSC.G 22 THERE ARE 22 CAPLUS RECORDS THAT CITE THIS RECORD (22 CITINGS)

RE.CNT 26 THERE ARE 26 CITED REFERENCES AVAILABLE FOR THIS RECORD  
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 29 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN

TI Comparing the properties of *Escherichia coli* branching enzyme and  
maize branching enzyme

AB *Escherichia coli* glycogen branching enzyme (GBE) and  
maize starch branching enzymes I (SBEI) and II (SBEII)  
were expressed in *E. coli* and purified. *E. coli* GBE branched amylose at a  
higher rate than did SBEII, but branched amylose at a lower rate than did  
SBEI. Similar to SBEI, GBE branched amylopectin at a lower rate than did  
SBEII. High-performance anion-exchange chromatog. anal. of the branched  
products produced by BE revealed the min. chain length (cl) required for  
branching. While GBE and SBEII showed the same min. cl [d.p. (dp) 12]  
required for branching, SBEI had a slightly higher min. cl (dp 16)  
requirement for branching. The major differences between GBE and SBE are  
their specificities in terms of the size of chains transferred. In  
comparison with SBE, GBE had a much narrower size range of chains  
transferred and transferred mainly shorter chains. While SBEI and SBEII

produced a large number of chains ranging from dp 6 to over dp 30, GBE predominantly transferred chains ranging from dp 5 to 16 and produced only a very small number of long chains with dp greater than 20. Although it has been reported that SBEI and SBEII preferentially transfer longer and shorter chains, resp. (1), this study further defines the differences between SBEI and SBEII in the size of chains transferred. SBEI predominantly transfers longer chains with dp greater than 10, while producing few shorter chains with dp 3 to 5. In contrast, SBEII preferentially transfers smaller chains with dp 3 to 9, with the most abundant chains being dp 6 and 7. The significance of min. chain-length requirement by SBE is discussed in setting the invariant size of amylopectin cluster size (9 nm).

AN 1997:347385 HCAPLUS <<LOGINID::20100610>>

DN 127:46831

OREF 127:8835a,8838a

TI Comparing the properties of Escherichia coli branching enzyme and maize branching enzyme

AU Guan, Hanping; Li, Ping; Imparl-Radosevich, Jennifer; Preiss, Jack; Keeling, Peter

CS ExSeed Genetics, Agronomy Dep., Iowa State Univ., Ames, IA, 50011, USA

SO Archives of Biochemistry and Biophysics (1997), 342(1), 92-98

CODEN: ABBIA4; ISSN: 0003-9861

PB Academic

DT Journal

LA English

OSC.G 43 THERE ARE 43 CAPLUS RECORDS THAT CITE THIS RECORD (43 CITINGS)

RE.CNT 28 THERE ARE 28 CITED REFERENCES AVAILABLE FOR THIS RECORD

ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 30 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN

TI Independent genetic control of maize starch-branching enzymes IIa and IIb. Isolation and characterization of a Sbe2a cDNA

AB In maize (Zea mays L.) three isoforms of starch-branching enzyme (SBEI, SBEIIa, and SBEIIb) are involved in the synthesis of amylopectin, the branched component of starch. To isolate a cDNA encoding SBEIIa, degenerate oligonucleotides based on domains highly conserved in Sbe2 family members were used to amplify Sbe2-family cDNA from tissues lacking SBEIIb activity. The predicted amino acid sequence of a Sbe2a cDNA matches the N-terminal sequence of SBEIIa protein purified from maize endosperm. The size of the mature protein deduced from the cDNA also matches that of SBEIIa. Features of the predicted protein are most similar to members of the SBEII family; however, it differs from maize SBEIIb in having a 49-amino acid N-terminal extension and a region of substantial sequence divergence. Sbe2a mRNA levels are 10-fold higher in embryonic than in endosperm tissue, and are much lower than Sbe2b in both tissues. Unlike Sbe2b, Sbe2a-hybridizing mRNA accumulates in leaf and other vegetative tissues, consistent with the known distribution of SBEIIa and SBEIIb activities.

AN 1997:332511 HCAPLUS <<LOGINID::20100610>>

DN 127:76709

OREF 127:14545a,14548a

TI Independent genetic control of maize starch-branching enzymes IIa and IIb. Isolation and characterization of a Sbe2a cDNA

AU Gao, Ming; Fisher, Dane K.; Kim, Kyung-Nam; Shannon, Jack C.; Gultinan, Mark J.

CS Biotechnology Inst., Pennsylvania State Univ., University Park, PA, 16802, USA

SO Plant Physiology (1997), 114(1), 69-78

CODEN: PLPHAY; ISSN: 0032-0889

PB American Society of Plant Physiologists

DT Journal  
 LA English  
 OSC.G 56 THERE ARE 56 CAPLUS RECORDS THAT CITE THIS RECORD (56 CITINGS)  
 RE.CNT 30 THERE ARE 30 CITED REFERENCES AVAILABLE FOR THIS RECORD  
 ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 31 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN  
 TI Isolation, characterization and expression analysis of a starch  
 branching enzyme II cDNA from wheat  
 AB A full-length cDNA (2970 bp) encoding a starch branching  
 enzyme II (SBEII; EC 2.4.1.18) in wheat (*Triticum aestivum* L. cv  
 Fielder) kernel was isolated from a cDNA library. The translated region  
 of the cDNA predicted a 823 amino acid primary product with a mol. mass of  
 91.4 kDa. A 54 amino acid transit peptide was postulated to be cleaved  
 from the pre-protein to give a 769 amino acid (85.4 kDa) mature  
 polypeptide, which showed extensive sequence similarity to SBEII sequences  
 characterized from maize, rice and pea. Expression of the  
 isolated cDNA in a BE-deficient *E. coli* strain demonstrated that it  
 encoded a functional BE. RNA anal. of *Sbe2* gene expression during seed  
 development revealed that *Sbe2* mRNA levels were highest in young kernels  
 (5-10 days post-anthesis) and declined as the kernels matured.

AN 1997:123840 HCAPLUS <<LOGINID::20100610>>  
 DN 126:248817  
 OREF 126:48055a,48058a  
 TI Isolation, characterization and expression analysis of a starch  
 branching enzyme II cDNA from wheat  
 AU Nair, Ramesh B.; Baga, Monica; Scoles, Graham J.; Kartha, Kutty K.;  
 Chibbar, Ravindra N.  
 CS Department of Crop Science and Plant Ecology, University of Saskatchewan,  
 Saskatoon, SK, S7N 5A8, Can.  
 SO Plant Science (Shannon, Ireland) (1997), 122(2), 153-163  
 CODEN: PLSCE4; ISSN: 0168-9452  
 PB Elsevier  
 DT Journal  
 LA English  
 OSC.G 30 THERE ARE 30 CAPLUS RECORDS THAT CITE THIS RECORD (30 CITINGS)

L8 ANSWER 32 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN  
 TI Molecular characterization of starch branching  
 enzyme genes, *sbe1*, *sbe2b* and *sbe2a* in maize (*Zea mays*  
 L.)  
 AB Unavailable  
 AN 1997:95523 HCAPLUS <<LOGINID::20100610>>  
 DN 126:115703  
 OREF 126:22309a,22312a  
 TI Molecular characterization of starch branching  
 enzyme genes, *sbe1*, *sbe2b* and *sbe2a* in maize (*Zea mays*  
 L.)  
 AU Gao, Ming  
 CS Pennsylvania State Univ., University Park, PA, USA  
 SO (1996) 108 pp. Avail.: Univ. Microfilms Int., Order No.  
 DA9702296  
 From: Diss. Abstr. Int., B 1997, 57(8), 4919  
 DT Dissertation  
 LA English

L8 ANSWER 33 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN  
 TI Differential expression and properties of starch-  
 branching enzyme isoforms in developing wheat endosperm  
 AB Three forms of starch-branching enzyme (BE)  
 from developing hexaploid wheat (*Triticum aestivum*) endosperm have been



partially purified and characterized. Immunol. cross-reactivities indicate that two forms (WBE-IAD, 88 kDa, and WBE-IB, 87 kDa) are related to the maize BE I class and that WBE-II (88 kDa) is related to maize BE II. Comparison of the N-terminal sequences from WBE-IAD and WBE-II with maize and rice BEs confirms these relationships. Evidence is presented from the anal. of nullisomic-tetrasomic wheat lines demonstrating that WBE-IB is located on chromosome 7B and that the WBE-IAD fraction contains polypeptides that are encoded on chromosomes 7A and 7D. The wheat endosperm BE classes are differentially expressed during endosperm development. WBE-II is expressed at a constant level throughout mid and late endosperm development. In contrast, WBE-IAD and WBE-IB are preferentially expressed in late endosperm development. Differences are also observed in the kinetic characteristics of the enzymes. The WBE-I isoforms have a 2- to 5-fold higher affinity for amylose than does WBE-II, and the WBE-I isoforms are activated up to 5-fold by phosphorylated intermediates and inorg. phosphate, whereas WBE-II is activated only 50%. The potential implications of this activation of BE I for starch biosynthesis are discussed.

AN 1997:73618 HCAPLUS <<LOGINID::20100610>>

DN 126:169149

OREF 126:32649a,32652a

TI Differential expression and properties of starch-branching enzyme isoforms in developing wheat endosperm

AU Morell, Matthew K.; Blennow, Andreas; Kosar-Hashemi, Behjat; Samuel, Michael S.

CS Cooperative Res. Cent. Plant Sci., Canberra, ACT 2601, Australia

SO Plant Physiology (1997), 113(1), 201-208

CODEN: PLPHAY; ISSN: 0032-0889

PB American Society of Plant Physiologists

DT Journal

LA English

OSC.G 90 THERE ARE 90 CAPLUS RECORDS THAT CITE THIS RECORD (90 CITINGS)

L8 ANSWER 34 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN

TI Evolutionary conservation and expression patterns of maize starch branching enzyme I and IIb genes suggest isoform specialization

AB Expression of the maize (*Zea mays* L.) starch branching enzyme (SBE) genes Sbe1 and Sbe2 were characterized during kernel development and in vegetative tissues. The onset of Sbe1 and Sbe2 expression during endosperm development was similar to that of other genes involved in starch biosynthesis (Wx, Sh2 and Bt2). However, the expression of Sbe2 peaked earlier than that of Sbe1 in developing endosperm and embryos resulting in a shift in the ratio of Sbe1 to Sbe2 relative message levels during kernel and embryo development. Transcripts hybridizing to the Sbe2 probe were not detectable in leaves kernel and embryo development. Transcripts hybridizing to the Sbe2 probe were not detectable in leaves or roots which nonetheless have SBEII enzymic activity, suggesting that there may be another divergent SBEII-like gene(s) in maize. A similar expression pattern is shared between the maize genes and related genes in pea, which together with their evolutionary conservation, suggests that the SBE isoforms may play unique roles in starch biosynthesis during plant development.

AN 1996:466120 HCAPLUS <<LOGINID::20100610>>

DN 125:137991

OREF 125:25725a

TI Evolutionary conservation and expression patterns of maize starch branching enzyme I and IIb genes suggest isoform specialization

AU Gao, Ming; Fisher, Dane K.; Kim, Kyung-Nam; Shannon, Jack C.; Guiltinan,

Mark J.  
CS Dep. of Horticulture, Pennsylvania State Univ., University Park, PA,  
16802, USA  
SO Plant Molecular Biology (1996), 30(6), 1223-1232  
CODEN: PMBIDB; ISSN: 0167-4412  
PB Kluwer  
DT Journal  
LA English  
OSC.G 52 THERE ARE 52 CAPLUS RECORDS THAT CITE THIS RECORD (52 CITINGS)

L8 ANSWER 35 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN  
TI Physical association of starch biosynthetic enzymes with starch granules  
of maize endosperm. Granule-associated forms of starch  
synthase I and starch branching enzyme II  
AB Antibodies were used to probe the degree of association of starch biosynthetic  
enzymes with starch granules isolated from maize (*Zea mays*)  
endosperm. Graded washings of the starch granule, followed by release of  
polypeptides by gelatinization in 2% sodium dodecyl sulfate, enables  
distinction between strongly and loosely adherent proteins. Mild aqueous  
washing of granules resulted in near-complete solubilization of  
ADP-glucose pyrophosphorylase, indicating that little, if any, ADP-glucose  
pyrophosphorylase is granule associated. In contrast, all of the waxy protein  
plus significant levels of starch synthase I and starch  
branching enzyme II (BEII) remained granule associated.  
Stringent washings using protease and detergent demonstrated that the waxy  
protein, more than 85% of total endosperm starch synthase I protein, and  
more than 45% of BEII protein were strongly associated with starch granules.  
Rates of polypeptide accumulation within starch granules remained constant  
during endosperm development. Soluble and granule-derived forms of BEII  
yielded identical peptide maps and overlapping tryptic fragments closely  
aligned with deduced amino acid sequences from BEII cDNA clones. These  
observations provide direct evidence that BEII exists as both soluble and  
granule-associated entities. Thus, it is concluded that each of the known  
starch biosynthetic enzymes in maize endosperm exhibits a  
differential propensity to associate with, or to become irreversibly  
entrapped within, the starch granule.

AN 1996:436720 HCAPLUS <<LOGINID::20100610>>  
DN 125:81944  
OREF 125:15407a,15410a  
TI Physical association of starch biosynthetic enzymes with starch granules  
of maize endosperm. Granule-associated forms of starch  
synthase I and starch branching enzyme II  
AU Mu-Forster, Chen; Huang, Rongmin; Powers, Joseph R.; Harriman, Robert W.;  
Knight, Mary; Singletary, George W.; Keeling, Peter L.; Wasserman, Bruce  
P.  
CS Dep. Food Sci., Rutgers Univ., New Brunswick, NJ, 08903-0231, USA  
SO Plant Physiology (1996), 111(3), 821-829  
CODEN: PLPHAY; ISSN: 0032-0889  
PB American Society of Plant Physiologists  
DT Journal  
LA English  
OSC.G 82 THERE ARE 82 CAPLUS RECORDS THAT CITE THIS RECORD (82 CITINGS)

L8 ANSWER 36 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN  
TI Two closely related cDNAs encoding starch branching  
enzyme from *Arabidopsis thaliana*  
AB Two starch branching enzyme (SBE) cDNAs were  
identified in an *Arabidopsis* seedling hypocotyl library using  
maize Sbe1 and Sbe2 cDNAs as probes. The two cDNAs have diverged  
5', and 3' ends, but encode proteins which share 90% identity over an  
extensive region with 70% identity to maize SBE IIb. Genomic

Southern blots suggest that the two cDNAs are the products of single, independent genes, and that addnl., more distantly related SBE genes may exist in the Arabidopsis genome. The two cDNAs hybridize to transcripts which show similar expression patterns in Arabidopsis vegetative and reproductive tissues, including seedlings, inflorescence rachis, mature leaves, and flowers. This is the first report of the identification of cDNAs encoding two closely related starch branching enzymes from the same species.

AN 1996:149142 HCAPLUS <<LOGINID::20100610>>

DN 124:224561

OREF 124:41433a,41436a

TI Two closely related cDNAs encoding starch branching enzyme from Arabidopsis thaliana

AU Fisher, Dane K.; Gao, Ming; Kim, Kyung-Nam; Boyer, Charles D.; Gultinan, Mark J.

CS Dep. Horticulture, Pennsylvania State Univ., Univ. Park, PA, 16802, USA

SO Plant Molecular Biology (1996), 30(1), 97-108

CODEN: PMBIDB; ISSN: 0167-4412

PB Kluwer

DT Journal

LA English

OSC.G 27 THERE ARE 27 CAPLUS RECORDS THAT CITE THIS RECORD (27 CITINGS)

L8 ANSWER 37 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN

TI Allelic analysis of the maize amylose-extender locus suggests

that independent genes encode starch-branching enzymes IIa and IIb

AB Starch branching enzymes (SBE) catalyze the formation of

$\alpha$ -1,6-glucan linkages in the biosynthesis of starch. Three distinct

SBE isoforms have been identified in maize (Zea mays L.)

endosperm, SBEI, Iia, and IIb. Independent genes have been identified

that encode maize SBEI and IIb; however, it has remained

controversial as to whether SBEIIa and IIb result from

post-transcriptional processes acting on the product of a single gene or

whether they are encoded by sep. genes. Thus, 16-isogenic lines carrying

independent alleles of the maize amylose-extender (ae) locus,

the structural gene for SBEIIb, were analyzed. At 22 days after

pollination ae-B1 endosperm expressed little She2b (ae)-hybridizing

transcript, and as expected, ae-B1 endosperm also lacked detectable SBEIIb

enzymic activity,. Also, ae-B1 endosperm contained SBEIIa enzymic

activity, strongly supporting the hypothesis that endosperm SBEIIa and IIb

are encoded by sep. genes. Furthermore, addition to encoding the predominant

Sbe2b-hybridizing message expressed in endosperm, the ae gene also encodes

the major She2b-like transcript expressed in developing embryos and

tassels.

AN 1996:119513 HCAPLUS <<LOGINID::20100610>>

DN 124:170828

OREF 124:31587a,31590a

TI Allelic analysis of the maize amylose-extender locus suggests

that independent genes encode starch-branching enzymes IIa and IIb

AU Fisher, Dane K.; Gao, Ming; Kim, Kyung-Nam; Boyer, Charles D.; Gultinan, Mark J.

CS Biotechnol. Inst., Pennsylvania State Univ., University Park, PA, 16802, USA

SO Plant Physiology (1996), 110(2), 611-19

CODEN: PLPHAY; ISSN: 0032-0889

PB American Society of Plant Physiologists

DT Journal

LA English

OSC.G 39 THERE ARE 39 CAPLUS RECORDS THAT CITE THIS RECORD (39 CITINGS)

L8 ANSWER 38 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN

TI Molecular genetic analysis of multiple isoforms of starch branching enzyme with emphasis on Zea mays L. (Arabidopsis thaliana)

AB Unavailable

AN 1996:103412 HCAPLUS <<LOGINID::20100610>>

DN 124:166805

OREF 124:30743a,30746a

TI Molecular genetic analysis of multiple isoforms of starch branching enzyme with emphasis on Zea mays L. (Arabidopsis thaliana)

AU Fisher, Dane Kinard

CS Pennsylvania State Univ., University Park, PA, USA

SO (1995) 185 pp. Avail.: Univ. Microfilms Int., Order No. DA9600172

From: Diss. Abstr. Int., B 1995, 56(9), 4707

DT Dissertation

LA English

L8 ANSWER 39 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN

TI Bt1, a structural gene for the major 39-44 kDa amyloplast membrane polypeptides

AB The relationship between the Bt1 gene (Bt1) and the major 39-44 kDa amyloplast membrane polypeptides which were deficient in amyloplast membranes of brittle1 (bt1) kernels of maize (Zea mays L.) was examined. A rapid yet gentle procedure for the isolation of amyloplasts from immature kernels is described. These amyloplasts were relatively free of contamination by other cellular components, and immunol. studies showed that they contained polypeptides which reacted with antibodies to maize starch branching enzyme and ADP-Glc pyrophosphorylase. Purified membranes isolated from the amyloplast contained a polypeptide which reacted with antibodies to the Pi-translocator from spinach chloroplasts. However, a cluster of 39-44 kDa polypeptides accounted for about 40% of the total amyloplast membrane protein from W64A kernels. These polypeptides were specifically recognized by antibodies raised against a fusion protein consisting of 56 amino acids of the carboxyl terminus of the BT1 protein and glutathione S-transferase. The BT1 antibodies also reacted with the abundant polypeptides in amyloplast membranes from hybrid kernels (Doebler 66XP and Pioneer 3780), and the shrunken1 and shrunken2 mutant genotypes, but no BT1 reacting polypeptides were present in amyloplast membranes from bt1 mutant kernels. BT1 was detected by the immunoblot procedure in microsomal membranes from embryo and pericarp tissues from the kernel, from seedling roots and shoots, or in membranes from mitochondria and chloroplasts. The same BT1 immunoblot pattern was obtained for proteins extracted from microsomal membranes from developing endosperm and from purified amyloplast membranes. A linear relationship between the number of copies of Bt1 alleles and the levels of BT1 in endosperm microsomal membranes was demonstrated in a gene dosage series. BT1 was not extracted from amyloplast membranes by chloroform/methanol or by alkaline buffer at pH 11.5, but was partially extracted by 0.1 M NaOH. Thus, Bt1 is the structural gene for the major 39-44 kDa amyloplast membrane polypeptides and these polypeptides are integral proteins specific to amyloplast membranes from the endosperm.

AN 1996:20003 HCAPLUS <<LOGINID::20100610>>

DN 124:50872

OREF 124:9531a,9534a

TI Bt1, a structural gene for the major 39-44 kDa amyloplast membrane polypeptides

AU Cao, Heping; Sullivan, Thomas D.; Boyer, Charles D.; Shannon, Jack C.

CS Dept Biochemistry, Michigan State Univ., East Lansing, MI, 48824, USA

SO Physiologia Plantarum (1995), 95(2), 176-86

CODEN: PHPLAI; ISSN: 0031-9317

PB Munksgaard

DT Journal

LA English

OSC.G 39 THERE ARE 39 CAPLUS RECORDS THAT CITE THIS RECORD (39 CITINGS)

L8 ANSWER 40 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN

TI A cDNA encoding starch branching enzyme I  
from maize endosperm

AB An apparently full-length cDNA for starch branching  
enzyme (EC 2.4.1.18) isoform I was isolated by screening with a  
PCR fragment derived from primers based on a previously isolated cDNA  
clone. The open reading frame codes for 822 amino acids, including a  
putative 63-amino acid transit peptide.

AN 1995:695609 HCAPLUS <<LOGINID::20100610>>

DN 123:162340

OREF 123:28731a,28734a

TI A cDNA encoding starch branching enzyme I  
from maize endosperm

AU Fisher, Dane K.; Kim, Kyung-Nam; Gao, Ming; Boyer, Charles D.; Gultinan,  
Mark J.

CS Dep. Horticulture, Pennsylvania State Univ., University Park, PA, 16802,  
USA

SO Plant Physiology (1995), 108(3), 1313-14

CODEN: PLPHAY; ISSN: 0032-0889

PB Dekker

DT Journal

LA English

OSC.G 22 THERE ARE 22 CAPLUS RECORDS THAT CITE THIS RECORD (22 CITINGS)

L8 ANSWER 41 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN

TI Effect of temperature on enzymes in the pathway of starch biosynthesis in  
developing wheat and maize grain

AB Soluble starch synthase (SSS) is shown to be a major site of control of flux  
through the pathway of starch synthesis in developing wheat and  
maize grain. Temps. above 25°C adversely affect flux, and  
therefore, limit yield. This process is linked to SSS which is heat  
sensitive. Two apparently different properties of SSS can be identified  
which differ in the period required before full activity is restored after  
heat treatment. First, enzyme rate is adversely affected by elevated  
temperature, an effect which is reversible on returning to a lower temperature

The

effect on enzyme rate was quantified using enzyme Q10 which was found to  
begin to be sub-optimal above 20°. Second, with a prolonged period  
of exposure to elevated temperature there is a loss of enzyme activity which is  
not freely reversible which we have termed thermal inactivation. Although  
this occurs at temps. in excess of 20° in wheat, higher temps. of  
more than 30° are needed in maize SSS. Elevated temperature  
did not affect the inherent stability or Q10 characteristics of other  
enzymes in the pathway of starch synthesis except for  
branching enzyme which might have minimal flux-control  
strength. SSS thermal inactivation may not be a major problem in field  
conditions for developing maize grain, because temps. rarely are  
high enough. However, it is suggested that the effect on enzyme Q10 is  
more physiol. relevant, since maize SSS is operating  
sub-optimally as temps. exceed 20°. Calcns. of the redns. in  
maize US corn-belt yield showed that significant yield improvement  
might be obtained by a 5° shift in the temperature optimum. Thus,  
selections for a more temperature tolerant form of maize SSS were  
conducted using enzyme Q10 as a selection tool. Of several hundred  
maize specimens screened, two were found to be significantly

different. However, attempts to use backcross breeding to transfer this trait from the tropical donor to another line have not yet succeeded.

AN 1995:473988 HCAPLUS <<LOGINID::20100610>>

DN 122:286717

OREF 122:52151a,52154a

TI Effect of temperature on enzymes in the pathway of starch biosynthesis in developing wheat and maize grain

AU Keeling, P. L.; Banisadr, R.; Barone, L.; Wasserman, B. P.; Singletary, G. W.

CS Applied Biology Project, ICI Seeds, Slater, IA, 50244, USA

SO Australian Journal of Plant Physiology (1994), 21(6), 807-27  
CODEN: AJPPCH; ISSN: 0310-7841

PB Commonwealth Scientific and Industrial Research Organization

DT Journal

LA English

OSC.G 28 THERE ARE 28 CAPLUS RECORDS THAT CITE THIS RECORD (28 CITINGS)

L8 ANSWER 42 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN

TI Starch branching enzymes belonging to distinct enzyme families are differentially expressed during pea embryo development

AB CDNA clones for two isoforms of starch branching enzyme (SBEI and SBEII) have been isolated from pea embryos and sequenced. The deduced amino acid sequences of pea SBEI and SBEII are closely related to starch branching enzymes of maize, rice, potato and cassava and a number of glycogen branching enzymes from yeast, mammals and several prokaryotic species. In comparison with SBEI, the deduced amino acid sequence of SBEII lacks a flexible domain at the N-terminus of the mature protein. This domain is also present in maize SBEII and rice SBEIII and resembles one previously reported for pea granule-bound starch synthase II (GBSSII). However, in each case it is missing from the other isoform of SBE from the same species. On the basis of this structural feature (which exists in some isoforms from both monocots and dicots) and other differences in sequence, SBEs from plants may be divided into two distinct enzyme families. There is strong evidence from our own and other work that the amylopectin products of the enzymes from these two families are qual. different. Pea SBEI and SBEII are differentially expressed during embryo development. SBEI is relatively highly expressed in young embryos while maximum expression of SBEII occurs in older embryos. The differential expression of isoforms which have distinct catalytic properties means that the contribution of each SBE isoform to starch biosynthesis changes during embryo development. Qual. measurement of amylopectin from developing and maturing embryos confirms that the nature of amylopectin changes during pea embryo development and that this correlates with the differential expression of SBE isoforms.

AN 1995:459734 HCAPLUS <<LOGINID::20100610>>

DN 123:136225

OREF 123:24081a,24084a

TI Starch branching enzymes belonging to distinct enzyme families are differentially expressed during pea embryo development

AU Burton, Rachel A.; Bewley, J. Derek; Smith, Alison M.; Bhattacharyya, Madan K.; Tatge, Helma; Ring, Steve; Bull, Vicky; Hamilton, William D. O.; Martin, Cathie

CS John Innes Centre, John Innes Institute, Norwich, NR4 7UH, UK

SO Plant Journal (1995), 7(1), 3-15  
CODEN: PLJUED; ISSN: 0960-7412

DT Journal

LA English

OSC.G 91 THERE ARE 91 CAPLUS RECORDS THAT CITE THIS RECORD (91 CITINGS)

L8 ANSWER 43 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN

TI Expression of branching enzyme II of maize endosperm in  
Escherichia coli

AB A cDNA clone encoding maize branching enzyme II (BEII) has been  
independently isolated from a maize endosperm cDNA library. The  
deduced protein sequence of maize BEII was compared with that of  
BE from diverse sources. The gene encoding mature BEII of maize  
endosperm has been expressed in E. coli using the T7 promoter. The  
expressed BEII was purified to near homogeneity so that amylolytic  
activity and bacterial BE could be completely eliminated from the BE  
preparation. The expressed enzyme showed very similar properties to those of  
bEII purified from developing maize endosperm. This result  
confirmed our earlier report that BEII had a lower rate of branching  
amylose and the rate of branching amylopectin was twice that of branching  
amylose. This study also showed a greater advantage of purifying BEII  
from the bacterial expression system than from developing maize  
endosperm. Most importantly, this study has established a useful tool to  
study the structure-function relationships of the maize BE using  
site-directed mutagenesis.

AN 1995:140589 HCAPLUS <<LOGINID::20100610>>

DN 123:4386

OREF 123:915a,918a

TI Expression of branching enzyme II of maize endosperm in  
Escherichia coli

AU Guan, Han Ping; Baba, Tadashi; Preiss, Jack

CS Department Biochemistry, Michigan State University, East Lansing, MI,  
48824, USA

SO Cellular and Molecular Biology (Paris) (1994), 40(7), 981-8

CODEN: CMOBEF; ISSN: 0145-5680

PB C.M.B. Association

DT Journal

LA English

OSC.G 24 THERE ARE 24 CAPLUS RECORDS THAT CITE THIS RECORD (24 CITINGS)

L8 ANSWER 44 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN

TI Genetic isolation, cloning, and analysis of a Mutator-induced, dominant  
antimorph of the maize amylose extender1 locus

AB The authors report the genetic identification, mol. cloning, and  
characterization of a dominant mutant at the amylose extender1 locus,  
Ael-5180. The identities of the authors' clones are corroborated by their  
ability to reveal DNA polymorphisms between seven wild-type revertants  
from Ael-5180 relative to the Ael-5180 mutant allele and between four of  
five independently derived, Mutator (Mu)-induced recessive ael alleles  
relative to their resp. wild-type progenitor alleles. The Ael-5180  
mutation is associated with two Mui insertions flanked by complex  
rearrangements of ael-related sequences. One of the Mui elements is  
flanked by inverted repeats of ael-related DNA of at least 5.0 kb in  
length. This Mui element and at least some of this flanking inverted  
repeat DNA are absent or hypermethylated in six of seven wild-type  
revertants of Ael-5180 that were analyzed. The second Mui element is  
flanked on one side by the 5.0-kb ael-specific repeat and on the other  
side by a sequence that does not hybridize to the ael-related repeat  
sequence. This second Mui element is present in revertants to the wild  
type and does not, therefore, appear to affect ael gene function. A  
2.7-kb ael transcript can be detected in wild-type and homozygous ael-Ref  
endosperms 20 days after pollination. This transcript is absent in  
endosperms containing one, two, or three doses of Ael-5180. This result is  
consistent with a suppression model to explain the dominant gene action of  
Ael-5180 and establishes Ael-5180 as an antimorphic allele. Homozygous  
wild-type seedlings produce no detectable transcript, indicating some  
degree of tissue specificity for ael expression. Sequence analyses  
establish that ael encodes starch branching

enzyme II.  
 AN 1994:550052 HCAPLUS <<LOGINID::20100610>>  
 DN 121:150052  
 OREF 121:26949a,26952a  
 TI Genetic isolation, cloning, and analysis of a Mutator-induced, dominant  
 antimorph of the maize amylose extender1 locus  
 AU Stinard, Philip S.; Robertson, Donald S.; Schnable, Patrick S.  
 CS Dep. Agron., Iowa State Univ., Ames, IA, 50011, USA  
 SO Plant Cell (1993), 5(11), 1555-66  
 CODEN: PLCEEW; ISSN: 1040-4651  
 DT Journal  
 LA English  
 OSC.G 62 THERE ARE 62 CAPLUS RECORDS THAT CITE THIS RECORD (62 CITINGS)

L8 ANSWER 45 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN  
 TI Modulating the quantity and quality of starch synthesis in plants by  
 placing the gene for a starch-metabolizing enzyme under control of a  
 regulated promoter  
 AB A method of producing a plant with switchable starch-synthesizing ability  
 by stably incorporating a target gene for an enzyme involved in a starch  
 or glycogen biosynthetic pathway and under the control of a regulated  
 promoter into the genome of a recipient plant. A plant with controllable  
 starch-synthesizing ability may have switchable starch yield, and/or  
 switchable starch quality. Starch or glycogen biosynthetic enzymes  
 include soluble starch synthase, branching enzyme  
 , glycogen synthase, ADP-glucose pyrophosphorylase, self-glucosylating  
 protein, glycogenin and amylogenin. DNA constructs for use in this method  
 are described, as well as plants transformed with said DNA constructs, the  
 seeds and progeny of such plants, and hybrids whose pedigree includes such  
 plants. The examples demonstrate the functioning of the chemical-inducible  
 promoter of the gene for the 27 kd subunit of glutathione-S-transferase II  
 in maize endosperm and discuss the construction of appropriate  
 expression vectors.

AN 1994:530242 HCAPLUS <<LOGINID::20100610>>  
 DN 121:130242  
 OREF 121:23445a,23448a  
 TI Modulating the quantity and quality of starch synthesis in plants by  
 placing the gene for a starch-metabolizing enzyme under control of a  
 regulated promoter  
 IN Keeling, Peter Lewis  
 PA Zeneca Ltd., UK  
 SO PCT Int. Appl., 52 pp.  
 CODEN: PIXXD2

DT Patent  
 LA English

FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
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PI	WO 9411520	A2	19940526	WO 1993-GB2305	19931109 <--
	WO 9411520	A3	19940804		
	W: AU, BB, BG, BR, BY, CA, CZ, FI, HU, JP, KP, KR, KZ, LK, LV, MG,				
	MN, MW, NO, NZ, PL, RO, RU, SD, SK, UA, US, VN				
	RW: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE,				
	BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG				
	AU 9454285	A	19940608	AU 1994-54285	19931109 <--
PRAI	GB 1992-23454	A	19921109	<--	
	WO 1993-GB2305	W	19931109	<--	

OSC.G 22 THERE ARE 22 CAPLUS RECORDS THAT CITE THIS RECORD (22 CITINGS)

RE.CNT 10 THERE ARE 10 CITED REFERENCES AVAILABLE FOR THIS RECORD  
 ALL CITATIONS AVAILABLE IN THE RE FORMAT



L8 ANSWER 46 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN

TI Expression of branching enzyme I of maize endosperm in  
Escherichia coli

AB The gene encoding for mature branching enzyme (BE) I (BEI) of  
maize (*Zea mays* L.) endosperm has been expressed in *Escherichia*  
*coli* using the T7 promoter. The expressed BEI was purified to near  
homogeneity so that amylolytic activity and bacterial BE could be  
completely eliminated from the BE preparation. The recombinant enzyme showed  
properties very similar to those of BEI purified from developing  
maize endosperm with respect to branching amylose and amylopectin.  
This result confirmed the authors' earlier report that maize  
endosperm BEI had a higher rate of branching amylose and a much lower rate  
(less than 10% of that of branching amylose) of branching amylopectin.  
This study also showed a great advantage in purifying BE from the  
bacterial expression system rather than from developing maize  
endosperm. Most important, this study has established the system with  
which to study the structure-function relationships of the maize  
BEI using site-directed mutagenesis.

AN 1994:502618 HCAPLUS <<LOGINID::20100610>>

DN 121:102618

OREF 121:18339a,18342a

TI Expression of branching enzyme I of maize endosperm in  
*Escherichia coli*

AU Guan, Han Ping; Baba, Tadashi; Preiss, Jack

CS Dep. Biochem., Michigan State Univ., East Lansing, MI, 48824, USA

SO Plant Physiology (1994), 104(4), 1449-53

CODEN: PLPHAY; ISSN: 0032-0889

DT Journal

LA English

OSC.G 31 THERE ARE 31 CAPLUS RECORDS THAT CITE THIS RECORD (31 CITINGS)

L8 ANSWER 47 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN

TI Differentiation of the properties of the branching isoenzymes from  
maize (*Zea mays*)

AB The multiple forms of branching enzyme (BE) from developing maize  
(*Zea mays*) endosperm were purified by modification of previous procedures  
such that amylase activity could be eliminated completely from the BE  
preparation. Three distinct assays for BE activity (phosphorylase a stimulation  
assay, BE linkage assay, and iodine stain assay) were used to characterize  
and differentiate the properties of the BE isoforms. This study presents  
the first evidence that the BE isoforms differ in their action on  
amylopectin. BEI had the highest activity in branching amylose, but its  
rate of branching amylopectin was less than 5% of that of branching  
amylose. Conversely, BEII isoforms had lower rates in branching amylose  
(about 9-12% of that of BEI) and had higher rates of branching amylopectin  
(about 6-fold) than BEI. The implication of these findings to the  
mechanism of amylopectin synthesis in vivo are discussed.

AN 1994:48576 HCAPLUS <<LOGINID::20100610>>

DN 120:48576

OREF 120:8791a,8794a

TI Differentiation of the properties of the branching isoenzymes from  
maize (*Zea mays*)

AU Guan, Han Ping; Preiss, Jack

CS Dep. Biochem., Michigan State Univ., East Lansing, MI, 48824, USA

SO Plant Physiology (1993), 102(4), 1269-73

CODEN: PLPHAY; ISSN: 0032-0889

DT Journal

LA English

OSC.G 113 THERE ARE 113 CAPLUS RECORDS THAT CITE THIS RECORD (113 CITINGS)

L8 ANSWER 48 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN

TI Starch branching enzyme II from  
maize endosperm

AB The authors report here the cloning of a SBE II cDNA from maize. Three  $\lambda$ gt10 cDNA libraries were constructed from endosperm poly(A)+ RNA 14, 22, and 29 DAP. A heterologous nucleic acid probe, clone pJSBE5, the cDNA for pea SBE I, was used to screen the 14-DAP library. After purifying and subcloning into plasmid pBluescript II SK- (Stratagene), a full-length cDNA of 2725 bp was isolated. Northern blots of total maize RNA isolated from endosperm tissue 12 DAP and probed with the cloned maize cDNA revealed a single transcript of approx. 2.7 kb. Deduced amino acid sequence was compared with the pea SBE I (Bhattacharya et al., 1990), maize SBE I (Baba et al., 1991), and rice SBE I (Nakamura et al., 1992) translated cDNA sequences using Intelligenetics software. Levels of residue identify were 71, 52, and 52%, resp. From these results, the authors conclude that they have cloned a second isoform of SBE from maize endosperm. This conclusion is supported by the N-terminal sequence of purified maize SBE IIb protein, which matches the cDNA predicted amino acid sequence at residues 58 to 65. The addnl. amino acid residues making up the N-terminal end of the deduced sequence are thought to encode a transit peptide (53 amino acids) for routing of the protein to the amyloplast. The deduced mol. weight of the mature protein from this sequence data is 84,772. This is slightly larger than size ests. of 80,000 D based upon SDS-PAGE anal. of purified SBE IIa and IIb protein (Boyer and Preiss, 1978; Singh and Preiss, 1985).

AN 1993:621872 HCAPLUS <<LOGINID::20100610>>  
DN 119:221872  
OREF 119:39477a,39480a

TI Starch branching enzyme II from  
maize endosperm

AU Fisher, Dane K.; Boyer, Charles D.; Hannah, L. Curtis  
CS Dep. Hortic., Pennsylvania State Univ., University Park, PA, 16802, USA  
SO Plant Physiology (1993), 102(3), 1045-6  
CODEN: PLPHAY; ISSN: 0032-0889

DT Journal  
LA English

OSC.G 63 THERE ARE 63 CAPLUS RECORDS THAT CITE THIS RECORD (64 CITINGS)

L8 ANSWER 49 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN

TI Starch branching enzyme cDNA from Solanum  
tuberosum

AB A full-length cDNA clone encoding starch branching enzyme (SBE, E.C. 2.4.1.18) was isolated from a Solanum tuberosum sprout cDNA library using a partial potato SBE cDNA clone that was originally isolated with a heterologous cDNA encoding a pea SBE. The 3114 bp DNA sequence revealed an ORF which encodes an 861 amino acid protein which has significant similarity to SBE I from maize and rice. The protein has a calculated Mr of 99,083. The SBE amino terminus has some features in common with chloroplast transit peptides, i.e. a high content of Ser and Thr residues and a central, pos. charged domain. Also, the hydropathicity profiles of the amyloplast transit peptide from the potato granule-bound starch synthase and the amino terminus of SBE are similar.

AN 1993:554604 HCAPLUS <<LOGINID::20100610>>  
DN 119:154604  
OREF 119:27569a,27572a

TI Starch branching enzyme cDNA from Solanum  
tuberosum

AU Poulsen, Peter; Kreiberg, Jette D.  
CS MARIBO Seed, Biotechnol., Copenhagen, DK-1001, Den.  
SO Plant Physiology (1993), 102(3), 1053-4  
CODEN: PLPHAY; ISSN: 0032-0889

DT Journal  
LA English  
OSC.G 26 THERE ARE 26 CAPLUS RECORDS THAT CITE THIS RECORD (26 CITINGS)

L8 ANSWER 50 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN  
TI Starch branching enzymes from immature rice seeds  
AB Four forms of branching enzyme, termed RBE1, RBE2 (a mixture of RBE2A and RBE2B), RBE3, and RBE4, were apparently separated by DEAE-cellulose column chromatog. of soluble extract from immature rice seeds, and each of these 4 forms was further purified by gel-filtration. RBE1, RBE2A, and RBE2B were the predominant forms of the enzyme. The mol. size, N-terminal amino acid sequence, and immunoreactivity with anti-maize branching enzyme-I (BE-I) antibody were identical among these 3 forms, except that the mol. mass of RBE2A was almost 3 kDa higher than those of RBE1 and RBE2B. These results indicate that RBE1, RBE2A, and RBE2B are the same; the enzyme is termed rice BE-I. The cDNA clones coding for rice BE-1 were identified from a rice seed library in  $\gamma$ gt11, using the maize BE-I cDNA as a probe. The nucleotide sequence indicates that rice BE-I is initially synthesized as an 820-residue precursor protein, including a putative 64- or 66-residue transit peptide at the N terminus. The rice mature BE-I contains 756 (or 754) amino acids with a calculated mol. mass of 86,734 (or 86,502) Da, and shares a high degree of sequence identity (86%) with the maize protein. The consensus sequences of the 4 regions that form the catalytic sites of amylolytic enzymes are conserved in the central region of the rice BE-I sequence. Thus, rice BE-I as well as the maize protein belongs to a family of amylolytic enzymes.

AN 1993:512080 HCAPLUS <<LOGINID::20100610>>

DN 119:112080

OREF 119:20053a,20056a

TI Starch branching enzymes from immature rice seeds

AU Mizuno, Kouichi; Kimura, Koji; Arai, Yuji; Kawasaki, Tsutomu; Shimada, Hiroaki; Baba, Tadashi

CS Inst. Appl. Biochem., Univ. Tsukuba, Tsukuba, 305, Japan

SO Journal of Biochemistry (1992), 112(5), 643-51

CODEN: JOBIAO; ISSN: 0021-924X

DT Journal

LA English

OSC.G 46 THERE ARE 46 CAPLUS RECORDS THAT CITE THIS RECORD (46 CITINGS)

L8 ANSWER 51 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN

TI Branching of amylose by the branching isoenzymes of maize endosperm

AB A convenient, quant. assay method of branching enzyme (BE) was devised with reduced amylose as the substrate. Using this assay, the properties of the purified branching isoenzymes from maize, BE I, IIa, and IIb, were studied. The method is based on determination of reducing power, by the

modified Park-Johnson method, of the chains transferred by BE after they are released from the branched products with isoamylase. The optimum pH of the three enzymes is 7.5, and the optimum temps. of BE I, IIa, and IIb are 33, 25, and 15-20°, resp. The specific activities are highest for BE I and the lowest for BE IIb, whereas in the conventional assay based on stimulation of unprimed phosphorylase activity, the specific activities are BE IIb > IIa > I. BE I has a lower Km (2.0  $\mu$ M of the nonreducing terminal) for the reduced amylose of average chain-length (.hivin.cl) 405 than BE IIa (10  $\mu$ M) and the IIb (11  $\mu$ M), and the enzyme shows a higher Km for reduced amyloses of smaller .hivin.cl. Gel-permeation chromatograms on Sephadex G-75SF of the chain transferred from the reduced amylose indicate that initially the three isoenzymes produced chains of various sizes (d.p. .apprx.8 to >200), and BE I

preferentially transfers longer chains than BE IIa and IIb.

AN 1993:186425 HCAPLUS <<LOGINID::20100610>>

DN 118:186425

OREF 118:31875a,31878a

TI Branching of amylose by the branching isoenzymes of maize  
endosperm

AU Takeda, Yasuhito; Guan, Han Ping; Preiss, Jack

CS Dep. Biochem., Michigan State Univ., East Lansing, MI, 48824, USA

SO Carbohydrate Research (1993), 240, 253-63

CODEN: CRBRAT; ISSN: 0008-6215

DT Journal

LA English

OSC.G 104 THERE ARE 104 CAPLUS RECORDS THAT CITE THIS RECORD (104 CITINGS)

L8 ANSWER 52 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN

TI Characterization of the (1 → 4)- $\alpha$ -D-glucan-branching  
6-glycosyltransferase by in vitro synthesis of branched starch  
polysaccharides

AB Starch branching enzyme (Q-enzyme; EC

2.4.1.18) (I), isolated from young, mature potato tubers and purified by  
(NH<sub>4</sub>)<sub>2</sub>SO<sub>4</sub> precipitation, hydrophobic chromatog., and size-exclusion chromatog.,  
was found to be completely free of phosphorylase (EC 2.4.1.1) and  
 $\alpha$ -amylase (EC 3.2.1.1) activities. I had a mol. weight of 64 kDa, was  
homogeneous in SDS-PAGE, was inhibited by 4 + 10<sup>-5</sup> M oxidized  
glutathione, and could be stored at -80° in the presence of SH  
group-reducing agents. The actions of I alone, and in combination with  
potato phosphorylase, on amylose, pea starch, potato amylose, potato  
amylopectin, and waxy maize was investigated. The combination  
gave high-mol.-weight polysaccharides, debranching of which yielded patterns  
of short and long chains similar to those of debranched amylopectin.  
Treatment of amylose with I resulted in a decrease in the average mol. weight

and

in the broadening of the mol. weight distribution; debranching of the product  
yielded a short-chain distribution pattern.

AN 1992:250852 HCAPLUS <<LOGINID::20100610>>

DN 116:250852

OREF 116:42415a,42418a

TI Characterization of the (1 → 4)- $\alpha$ -D-glucan-branching  
6-glycosyltransferase by in vitro synthesis of branched starch  
polysaccharides

AU Praznik, Werner; Rammesmayr, Gerald; Spies, Thomas

CS Inst. Chem., Univ. Bodenkul., Vienna, A-1180, Austria

SO Carbohydrate Research (1992), 227, 171-82

CODEN: CRBRAT; ISSN: 0008-6215

DT Journal

LA English

OSC.G 7 THERE ARE 7 CAPLUS RECORDS THAT CITE THIS RECORD (7 CITINGS)

L8 ANSWER 53 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN

TI Comparison of soluble starch synthases and branching enzymes from leaves  
and kernels of normal and amylose-extender maize

AB Soluble starch synthases (SS) and branching enzymes (BE) from 20-day-old  
maize leaves and 22-day-old seeds of normal and amylose-extender  
(ae) were purified by DEAE-cellulose chromatog. Elution profiles of leaf  
exts. showed 1 major SS and 2 BE fractions from both genotypes. The SS  
fractions from normal and ae leaf exts. were capable of citrate-stimulated  
starch synthesis and had different reaction rates with various primers.  
The 2 BE fractions from normal leaf exts. differed significantly from each  
other but not when compared to the same BE from ae. Comparison of BE  
fractions from ae and normal leaves showed no differences based on  
chromatog., kinetic, and immunol. properties. Comparison of the leaf

enzymes with endosperm enzymes showed major differences. Leaf exts. did not contain SSII or BEIIb observed in endosperm exts. Developing ae endosperm lacked BEIIb activity and ae was the structural gene for BEIIb. The tissue-specific expression of BEIIb in the endosperm provided the basis for explaining the tissue-specific expression of ae. It was proposed that as BEIIb is expressed in the endosperm, but not leaves, allelic substitution at the ae locus modifies only endosperm starch synthesis.

AN 1990:94355 HCAPLUS <<LOGINID::20100610>>

DN 112:94355

OREF 112:15955a,15958a

TI Comparison of soluble starch synthases and branching enzymes from leaves and kernels of normal and amylose-extender maize

AU Dang, Peter L.; Boyer, Charles D.

CS Dep. Hort., Pennsylvania State Univ., University Park, PA, 16802, USA

SO Biochemical Genetics (1989), 27(9-10), 521-32

CODEN: BIGEBA; ISSN: 0006-2928

DT Journal

LA English

OSC.G 7 THERE ARE 7 CAPLUS RECORDS THAT CITE THIS RECORD (7 CITINGS)

L8 ANSWER 54 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN

TI The wrinkled-seed character of pea described by Mendel is caused by a transposon-like insertion in a gene encoding starch-branching enzyme

AB The r (rugosus) locus of pea (*Pisum sativum* L.), which detes. whether the seed is round or wrinkled, was cloned. Wrinkled (rr) seeds lack one isoform of starch-branching enzyme (SBEI), present in round (RR or Rr) seeds. A major polymorphism in the SBEI gene between near-isogenic RR and rr lines shows 100% cosegregation with the r locus, establishing that the SBEI gene is at the r locus. An aberrant transcript for SBEI is produced in rr embryos. In rr lines, the SBEI gene is interrupted by an 0.8 kb insertion that is very similar to the Ac/Ds family of transposable elements from maize. Failure to produce SBEI has complex metabolic consequences on starch, lipid, and protein biosynthesis in the seed.

AN 1990:93044 HCAPLUS <<LOGINID::20100610>>

DN 112:93044

OREF 112:15703a,15706a

TI The wrinkled-seed character of pea described by Mendel is caused by a transposon-like insertion in a gene encoding starch-branching enzyme

AU Bhattacharyya, Madan K.; Smith, Alison M.; Ellis, T. H. Noel; Hedley, Cliff; Martin, Cathie

CS John Innes Inst., AFRC Inst. Plant Sci. Res., Norwich, NR4 7UH, UK

SO Cell (Cambridge, MA, United States) (1990), 60(1), 115-22

CODEN: CELLB5; ISSN: 0092-8674

DT Journal

LA English

OSC.G 110 THERE ARE 110 CAPLUS RECORDS THAT CITE THIS RECORD (110 CITINGS)

L8 ANSWER 55 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN

TI Immunological comparison of the starch branching enzymes from potato tubers and maize kernels

AB Starch branching enzyme was purified from potato (*Solanum tuberosum*) tubers as a single species of 79 kilodaltons and specific antibodies were prepared against both the native enzyme and against the gel-purified, denatured enzyme. The activity of potato branching enzyme could only be neutralized by antinative potato branching enzyme, whereas both types of antibodies reacted with denatured potato branching enzyme. Starch branching enzymes were also isolated from

maize (*Zea mays*) kernels. All of the denatured forms of the maize enzyme reacted with antidenatured potato branching enzyme, whereas recognition by antinative potato branching enzyme was limited to maize branching enzymes I and IIb. Antibodies directed against the denatured potato enzyme were unable to neutralize the activity of any of the maize branching enzymes. Antinative potato branching enzyme fully inhibited the activity of maize branching enzyme I; the neutralized maize enzyme was identified as a 82 kilodalton protein. Thus, potato branching enzyme ( $M_r = 79,000$ ) shares a high degree of similarity with maize branching enzyme I ( $M_r = 82,000$ ), in the native as well as the denatured form. Cross-reactivity between potato branching enzyme and the other forms of maize branching enzyme was observed only after denaturation, which suggests mutual sequence similarities between these species.

AN 1989:454197 HCAPLUS <<LOGINID::20100610>>

DN 111:54197

OREF 111:9149a,9152a

TI Immunological comparison of the starch branching enzymes from potato tubers and maize kernels

AU Vos-Scheperkeuter, Greetje H.; De Wit, Janny G.; Ponstein, Anne S.; Feenstra, Will J.; Witholt, Bernard

CS Dep. Biochem., Groningen Biotechnol. Cent., Groningen, 9747 AG, Neth.

SO Plant Physiology (1989), 90(1), 75-84

CODEN: PLPHAY; ISSN: 0032-0889

DT Journal

LA English

OSC.G 11 THERE ARE 11 CAPLUS RECORDS THAT CITE THIS RECORD (11 CITINGS)

L8 ANSWER 56 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN

TI Maize leaf and kernel starch synthases and starch branching enzymes

AB Soluble starch synthases and branching enzymes were partially purified from developing leaves and kernels of maize using DEAE-cellulose chromatog. One form of starch synthase and 2 forms of branching enzyme were detected in leaves as compared to 2 forms of starch synthase and 3 forms of branching enzyme isolated from the kernels. The starch synthase fraction from the leaves and the 1st starch synthase fraction from the kernels showed greater activity in reactions containing various glycogens as primers than in those containing amylopectin. In addition, both were capable

of

synthesizing a polyglucan in the absence of an added primer but in the presence of Na citrate and bovine serum albumin (citrate-stimulated starch synthesis). The 2nd starch synthase fraction from kernels showed greater activity with amylopectin as primer and had no citrate-stimulated activity. The leaf enzyme and endosperm starch synthase I are suggested to be the same enzyme and constitutively expressed. Branching enzymes from leaves and kernels differed not only in their elution profiles but also their stimulation of phosphorylase a (assay A) and amylose branching (assay B) activities. A minor branching enzyme fraction from leaves (leaf branching enzyme I) eluted from the DEAE-cellulose column after the addition of a salt gradient, whereas branching enzyme I from kernels eluted in the buffer wash prior to the application of the gradient. However, the ratios of assay A to assay B suggested that branching enzyme I from leaves was catalytically similar to branching enzyme I from the kernels. The major leaf branching enzyme (branching enzyme II) eluted at the same position from the DEAE-cellulose column as endosperm branching enzyme IIa. These enzymes had similar ratios of activity (assay A/assay B). The cross-reaction of leaf branching enzymes with antisera prepared against maize endosperm branching enzymes in immunodiffusion expts. and enzyme activity neutralization expts. further demonstrated the relationship of the leaf and endosperm branching enzymes.

AN 1988:434288 HCAPLUS <<LOGINID::20100610>>  
DN 109:34288  
OREF 109:5733a,5736a  
TI Maize leaf and kernel starch synthases and starch branching  
enzymes  
AU Dang, Peter L.; Boyer, Charles D.  
CS Dep. Hortic., Pennsylvania State Univ., University Park, PA, 16802, USA  
SO Phytochemistry (1988), 27(5), 1255-9  
CODEN: PYTCAS; ISSN: 0031-9422  
DT Journal  
LA English  
OSC.G 20 THERE ARE 20 CAPLUS RECORDS THAT CITE THIS RECORD (20 CITINGS)

L8 ANSWER 57 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN  
TI Enzyme activities associated with maize kernel amyloplasts  
AB Activities of the enzymes of gluconeogenesis and of starch metabolism were measured in exts. of amyloplasts isolated from protoplasts derived from 14-day old maize (Zea mays cv Pioneer 3780) endosperm. The enzymes triosephosphate isomerase, fructose-1,6-bisphosphate aldolase, fructose-1,6-bisphosphatase, phosphohexose isomerase, phosphoglucomutase, ADPG pyrophosphorylase, UDPG pyrophosphorylase, soluble and bound starch synthases, and branching enzyme were present in the amyloplasts. Of the above enzymes, ADPG pyrophosphorylase had the lowest activity per amyloplast. Invertase, sucrose synthase, and hexokinase were not detected in similar amyloplast prepns. Only a trace of the cytoplasmic marker enzyme alc. dehydrogenase could be detected in purified amyloplast fractions. Also, purified amyloplasts were lysed and then supplied with radioactive glucose-6-phosphate, glucose-1-phosphate, fructose-1,6-bisphosphate, dihydroxyacetone phosphate, glucose, fructose, sucrose, and 3-O-methylglucose in the presence of ATP or uridine triphosphate. Of the above, only the phosphorylated substrates were incorporated into starch. Incorporation into starch was higher with added uridine triphosphate than with ATP. Dihydroxyacetone phosphate was the preferred substrate for uptake by intact amyloplasts and incorporation into starch. In preliminary expts., it appeared that glucose-6-P and fructose-1,6-bisphosphate may also be taken up by intact amyloplasts. However, the rate of uptake and incorporation into starch was relatively low and variable. Addnl. study is needed to determine conclusively whether hexose phosphates will cross intact amyloplast membranes. Thus: (a) triose phosphate is the preferred substrate for uptake by intact amyloplasts; (b) amyloplasts contain all enzymes necessary to convert triose phosphates into starch; (c) sucrose breakdown must occur in the cytosol prior to carbohydrate transfer into the amyloplasts; (d) under the conditions of assay, amyloplasts are unable to convert glucose or fructose to starch; (e) uridine triphosphate may be the preferred nucleotide for conversion of hexose phosphates to starch at this stage of kernel development.

AN 1988:201823 HCAPLUS <<LOGINID::20100610>>  
DN 108:201823  
OREF 108:33085a,33088a  
TI Enzyme activities associated with maize kernel amyloplasts  
AU Echeverria, Edgardo; Boyer, Charles D.; Thomas, Paul A.; Liu, Kang Chien; Shannon, Jack C.  
CS Dep. Hortic., Pennsylvania State Univ., University Park, PA, 16802, USA  
SO Plant Physiology (1988), 86(3), 786-92  
CODEN: PLPHAY; ISSN: 0032-0889  
DT Journal  
LA English  
OSC.G 16 THERE ARE 16 CAPLUS RECORDS THAT CITE THIS RECORD (16 CITINGS)

L8 ANSWER 58 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN

TI Biosynthesis of starch; identification of potato starch enzymes  
 AB Two important starch enzymes, granule-bound starch synthase and branching enzyme, were purified from potato tubers and characterized by immunol. comparison with the corresponding enzymes of other plants. Granule-bound starch synthase was identified as a 60-kilodalton (kd) protein homologous to the corresponding enzymes of maize and amaranth; the enzyme was missing in amylose-free potato starch granules. Branching enzyme of potato tubers was purified as a single protein species of 79 kd which appeared to be homologous to maize branching enzyme I, but much less to branching enzymes IIa and IIb.  
 AN 1988:127390 HCAPLUS <<LOGINID::20100610>>  
 DN 108:127390  
 OREF 108:20801a,20804a  
 TI Biosynthesis of starch; identification of potato starch enzymes  
 AU Vos-Scheperkeuter, G. H.; Ponstein, A. S.; De Wit, J. G.; Feenstra, W. J.; Oostergetel, G. T.; Van Bruggen, E. F. J.; Witholt, B.  
 CS Dep. Biochem., Groningen Biotechnol. Cent., Groningen, 9747 AG, Neth.  
 SO Food Hydrocolloids (1987), 1(5-6), 387-91  
 CODEN: FOHYES; ISSN: 0268-005X  
 DT Journal  
 LA English  
  
 L8 ANSWER 59 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN  
 TI Regulation of starch synthesis in Zea mays leaves  
 AB The kinetic properties of bundle sheath and mesophyll-specific ADP-glucose pyrophosphorylases (I) were studied with respect to the known localization of starch biosynthesis in the bundle sheath cells of maize. At least 75% of starch synthase and branching enzyme and 95% of I were in the bundle sheath; starch-degrading enzymes were more evenly distributed between cell types. Partially purified I from the 2 cell types were characterized by pH optima, substrate affinities, and regulatory properties. The bundle sheath enzyme was activated by 3-phosphoglycerate and other organic phosphates to a greater extent than was the mesophyll enzyme, and the bundle sheath enzyme was also less sensitive to phosphate inhibition. Thus, in vivo activity of maize leaf I as well as starch synthesis may be controlled by the levels of the enzymes in specific cell types and by the allosteric properties of I.  
 AN 1987:493580 HCAPLUS <<LOGINID::20100610>>  
 DN 107:93580  
 OREF 107:15227a,15230a  
 TI Regulation of starch synthesis in Zea mays leaves  
 AU Spilatro, Steven R.; Preiss, Jack  
 CS Dep. Biochem., Michigan State Univ., East Lansing, MI, 48824, USA  
 SO Prog. Photosynth. Res., Proc. Int. Congr. Photosynth., 7th (1987), Meeting Date 1986, Volume 3, 701-4. Editor(s): Biggins, John. Publisher: Nijhoff, Dordrecht, Neth.  
 CODEN: 55RQAT  
 DT Conference  
 LA English  
  
 L8 ANSWER 60 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN  
 TI Localization of starch biosynthetic and degradative enzymes in maize leaves  
 AB The cellular distribution of the starch biosynthetic and degradative enzymes in protoplasts prepared from maize (Zea mays) leaf mesophyll and bundle sheath cells was investigated. In conformity with the cellular distribution of starch, starch biosynthetic enzymes (soluble starch synthase, ADP glucose pyrophosphorylase, branching enzyme, and starch phosphorylase) were exclusively



localized in the bundle sheath cells. In contrast, starch degradative enzymes ( $\alpha$ -amylase,  $\beta$ -amylase, and debranching enzyme) were present in both types of leaf cells. Isolated chloroplasts from bundle sheath cells contained 100% of the starch biosynthetic enzymes. However, .apprx.60% of the activity of degradative enzymes and 67% of the activity of starch phosphorylase was localized in bundle sheath chloroplasts.

AN 1986:222052 HCAPLUS <<LOGINID::20100610>>

DN 104:222052

OREF 104:35153a,35156a

TI Localization of starch biosynthetic and degradative enzymes in maize leaves

AU Echeverria, Edgardo; Boyer, Charles D.

CS Dep. Hortic., Pennsylvania State Univ., University Park, PA, 16802, USA

SO American Journal of Botany (1986), 73(2), 167-71

CODEN: AJBOAA; ISSN: 0002-9122

DT Journal

LA English

OSC.G 11 THERE ARE 11 CAPLUS RECORDS THAT CITE THIS RECORD (11 CITINGS)

L8 ANSWER 61 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN

TI Starch branching enzymes from maize. Immunological characterization using polyclonal and monoclonal antibodies

AB Spleen cells from mice immunized with starch-branching enzymes were fused with cells from the mouse myeloma Sp2/0-AG14 cell line to form hybridomas. Those hybridomas producing antibodies against the branching enzyme were screened by the ELISA using purified branching enzyme as the antigen. Three monoclonal cell lines (1A1D7, 1A1C3, and 4D2A9D8) were found to produce antibodies which showed pos. ELISA reactions with maize branching enzyme I in addition to branching enzymes IIa and IIb. Three other monoclonal cell lines (4D2D10, 4D2F9, and 2A6C12) were also selected which produced antibodies showing pos. ELISA reactions with branching enzymes IIa and IIb only. The amino acid composition and peptide maps obtained after trypsin or chymotrypsin digestion show that there is no difference between branching enzymes IIa and IIb, but they are significantly different from branching enzyme I, which, along with immunol. data, suggests that only 2 forms of starch-branching enzyme may be present in maize kernels. Immunol. cross-reaction was also found between the starch-branching enzyme from maize kernels and the glycogen-branching enzyme from Escherichia coli, using polyclonal antibodies against starch-branching enzyme I or IIa and IIb or E. coli glycogen-branching enzyme, suggesting some immunol. similarities between maize starch-branching enzymes and E. coli glycogen-branching enzyme.

AN 1985:591998 HCAPLUS <<LOGINID::20100610>>

DN 103:191998

OREF 103:30836h,30837a

TI Starch branching enzymes from maize. Immunological characterization using polyclonal and monoclonal antibodies

AU Singh, Bijay K.; Preiss, Jack

CS Dep. Biochem. Biophys., Univ. California, Davis, CA, 95616, USA

SO Plant Physiology (1985), 79(1), 34-40

CODEN: PLPHAY; ISSN: 0032-0889

DT Journal

LA English

OSC.G 10 THERE ARE 10 CAPLUS RECORDS THAT CITE THIS RECORD (10 CITINGS)

L8 ANSWER 62 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN

TI Immunological characterization of maize starch branching enzymes

AB Highly purified fractions of 3 starch-branching enzymes from developing maize endosperm were used to prepare antisera in rabbits. In double

diffusion expts., no immunoppt. was observed when branching enzyme IIa or IIb was tested against branching enzyme I antiserum. No immunoppt. was formed when branching enzyme I was tested against branching enzyme IIa or IIb antiserum. Increasing amts. of antisera in the above combinations also failed to inhibit enzyme activity. Branching enzyme IIa antiserum cross-reacted and formed spurs with branching enzyme IIb when compared with branching enzyme IIa antigen. Comparison of branching enzyme IIb antiserum with branching enzyme IIa also resulted in an immunoppt. Increasing levels of branching enzyme IIa antiserum inhibited branching enzyme IIb as did the reciprocal combination. Thus, branching enzymes IIa and IIb are immunol. similar, whereas branching enzyme I is distinct. The data supports the classification of starch-branching enzymes based on genetic, kinetic, and chromatog. properties.

AN 1983:484351 HCAPLUS <<LOGINID::20100610>>

DN 99:84351

OREF 99:12965a,12968a

TI Immunological characterization of maize starch branching enzymes

AU Fisher, Mary B.; Boyer, Charles D.

CS Dep. Hortic., Pennsylvania State Univ., University Park, PA, 16802, USA

SO Plant Physiology (1983), 72(3), 813-16

CODEN: PLPHAY; ISSN: 0032-0889

DT Journal

LA English

OSC.G 6 THERE ARE 6 CAPLUS RECORDS THAT CITE THIS RECORD (6 CITINGS)

L8 ANSWER 63 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN

TI Gene dosage at the amylose-extender locus of maize: effects on the levels of starch branching enzymes

AB Soluble starch-branching enzymes and starch synthases from corn kernels of differing dosage of the ae locus were purified by DEAE-cellulose chromatog. A near-linear relation between increasing dosage of the dominate amylose-extender allele (Ae) and branching enzyme IIb activity was found. In contrast, levels and properties of branching enzymes I and IIa, as well as the citrate-stimulated and primer-requiring starch synthases, remained unchanged. The near-linear increase in branching enzyme IIb activity with increasing doses of the Ae allele is consistent with the hypothesis that ae is the structural gene coding for branching enzyme IIb.

AN 1982:488902 HCAPLUS <<LOGINID::20100610>>

DN 97:88902

OREF 97:14769a,14772a

TI Gene dosage at the amylose-extender locus of maize: effects on the levels of starch branching enzymes

AU Hedman, Karen D.; Boyer, Charles D.

CS Dep. Hortic. For., Rutgers, State Univ., New Brunswick, NJ, 08903, USA

SO Biochemical Genetics (1982), 20(5-6), 483-92

CODEN: BIGEBA; ISSN: 0006-2928

DT Journal

LA English

OSC.G 16 THERE ARE 16 CAPLUS RECORDS THAT CITE THIS RECORD (16 CITINGS)

L8 ANSWER 64 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN

TI Evidence for independent genetic control of the multiple forms of maize endosperm branching enzymes and starch synthases

AB Soluble starch synthase and starch-branching enzymes in exts. from kernels of 4 corn genotypes were compared. Exts. from normal (nonmutant) corn were found to contain 2 starch synthases and 3 branching enzyme fractions. The different fractions could be distinguished by chromatog. properties and kinetic properties under various assay conditions. Kernels homozygous for the recessive amylose-extender (ae) allele were missing branching enzyme IIb. In addition, the

citrate-stimulated activity of starch synthase I was reduced. This activity could be regenerated by the addition of branching enzyme to this fraction. No other starch synthase fractions were different from normal enzymes. Exts. from kernels homozygous for the recessive dull (du) allele were found to contain lower branching enzyme IIa and starch synthase II activities. Other fractions were not different from the normal enzymes. Anal. of exts. from kernels of the double mutant ae du indicated that the 2 mutants act independently. Branching enzyme IIb was absent and the citrate-stimulated reaction of starch synthase I was reduced but could be regenerated by the addition of branching enzyme (ae properties) and both branching enzyme IIa and starch synthase II were greatly reduced (du properties). Starch from ae and du endosperms contains higher amylose (66 and 42%, resp.) than normal endosperm (26%). In addition, the amylopectin fraction of ae starch is less highly branched than amylopectin from normal or du starch. The above observations suggest that the alterations of the starch may be accounted for by changes in the soluble synthase and branching enzyme fractions.

AN 1981:458224 HCAPLUS <<LOGINID::20100610>>

DN 95:58224

OREF 95:9805a,9808a

TI Evidence for independent genetic control of the multiple forms of maize endosperm branching enzymes and starch synthases

AU Boyer, Charles D.; Preiss, Jack

CS Dep. Biochem. Biophys., Univ. California, Davis, CA, 95616, USA

SO Plant Physiology (1981), 67(6), 1141-5

CODEN: PLPHAY; ISSN: 0032-0889

DT Journal

LA English

OSC.G 56 THERE ARE 56 CAPLUS RECORDS THAT CITE THIS RECORD (56 CITINGS)

L8 ANSWER 65 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN

TI Evidence for independent genetic control of the multiple forms of maize endosperm branching enzymes and starch synthases

AB Two forms of starch synthase (EC 2.4.1.21) were isolated from an (NH<sub>4</sub>)<sub>2</sub>SO<sub>4</sub> fraction of dent maize endosperm extract by DEAE-cellulose chromatog. Synthase I had higher activity with glycogen than amylopectin as a primer, whereas synthase II had higher activity with amylopectin. Both enzyme had a Km for ADP-glucose of 0.10 mM. Three forms of branching enzyme (EC 2.4.1.18) were also separated from maize endosperm on DEAE-cellulose. Fraction I was observed in the void volume, whereas fractions IIa and IIb coeluted with starch synthase I and II, resp. These enzymes were examined in 2 maize mutants with altered starch structure. Starch from amylose-extender (ae) mutant endosperm contained a higher proportion of linear amylose and amylopectin with fewer branch points than normal amylopectin. Normal starch synthase I and II levels were observed in ae mutants, but most if not all branching enzyme activity associated with starch synthase I was missing. The dull mutant, which also contains a higher than normal proportion of amylose, contained normal levels of starch synthase I and branching enzyme I but a significant (60%) decrease in starch synthase II activity and a small decrease in branching enzyme activity associated with starch synthase II fractions was observed

AN 1981:420241 HCAPLUS <<LOGINID::20100610>>

DN 95:20241

OREF 95:3500h,3501a

TI Evidence for independent genetic control of the multiple forms of maize endosperm branching enzymes and starch synthases

AU Preiss, Jack; Boyer, Charles D.

CS Dep. Biochem. Biophys., Univ. California, Davis, CA, USA

SO Mech. Saccharide Polym. Depolym., [Proc. Symp.] (1980), Meeting  
Date 1978, 161-74. Editor(s): Marshall, James John. Publisher: Academic,  
New York, N. Y.  
CODEN: 45MHAY

DT Conference

LA English

OSC.G 6 THERE ARE 6 CAPLUS RECORDS THAT CITE THIS RECORD (6 CITINGS)

L8 ANSWER 66 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN

TI The citrate-stimulated starch synthase of starchy maize kernels:  
purification and properties

AB Chromatog. of the maize kernel exts. on DEAE-cellulose resolves  
2 fractions of starch synthase activity, one of which (starch synthase I)  
is capable of synthesizing  $\alpha$ -glucan in the absence of exogenous  
primer and the presence of 0.5M citrate (J. L. Ozbun, et al., 1971). This  
starch synthase was purified 200-fold from developing kernels of normal  
maize, and shown to have no detectable activities of branching  
enzyme, amylase, pullulanase, phosphorylase, or D enzyme. The preparation,  
however, was not electrophoretically homogeneous. This preparation had a  $K_m$  of  
0.033 mM for ADP/glucose in the presence of 0.05M citrate. The reaction  
in the presence of citrate was stimulated 10-fold by the addition of excess  
purified branching enzyme. This stimulation is higher than those reported  
previously, but is consistent with the predicted effects of removal of  
amylase activity. The effects of salts other than citrate on activity in  
the absence of exogenous primer were small, but the stimulation could be  
restored by the addition of excess purified branching enzyme. Citrate  
increased the affinity of the enzyme for the endogenous primer present to  
such a level that no effect of exogenous primer on reaction rate could be  
observed in the presence of 0.5M citrate. Anal. of the glucan-iodine complex  
and the enzymic breakdown products patterns from the products of the  
starch synthase reaction indicates a high degree of linearity. The  
results obtained are discussed in relation to the biosynthesis of starch  
in vivo.

AN 1980:599890 HCAPLUS <<LOGINID::20100610>>

DN 93:199890

OREF 93:31814h,31815a

TI The citrate-stimulated starch synthase of starchy maize kernels:  
purification and properties

AU Pollock, Christopher; Preiss, Jack

CS Dep. Biochem. Biophys., Univ. California, Davis, CA, 95616, USA

SO Archives of Biochemistry and Biophysics (1980), 204(2), 578-88

CODEN: ABBIA4; ISSN: 0003-9861

DT Journal

LA English

OSC.G 24 THERE ARE 24 CAPLUS RECORDS THAT CITE THIS RECORD (24 CITINGS)

L8 ANSWER 67 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN

TI Properties of citrate-stimulated starch synthesis catalyzed by starch  
synthase I of developing maize kernels

AB Starch synthase I, purified .apprx.1000-fold from corn kernels homozygous  
for the endosperm mutant amylose-extender (ae), was capable of synthesis  
in the absence of added primer and in the presence of 0.5 M citrate.  
Because ae endosperm lacks the starch-branching  
enzyme which normally purifies with starch synthase I,  
the final enzyme fraction derived was free of detectable branching  
activity, permitting a detailed characterization of the citrate-stimulated  
reaction. This reaction was dependent on citrate concns. of >0.1 M. The  
reaction was not specific for citrate, however, since malate also  
stimulated the reaction. Branching enzyme increased the velocity of the  
reaction .apprx.4-fold, but did not replace the requirement for citrate.  
The  $K_m$  values for the primers amylopectin and glycogen were lowered by

citrate from 122 and 595 to 6 and 50 µg/mL, resp. The enzyme contained 1.7 mg of anhydroglucose units/enzyme unit. Thus, reaction mixts. contained 1-5 µg (5-25 µg/mL) of endogenous primer. The citrate-stimulated reaction may be explained as an increased affinity for this endogenous primer. The starch synthase reaction in the absence of primer was dependent on several factors, including endogenous primer concentration, citrate concentration, and branching enzyme concentration

AN 1980:72789 HCAPLUS <<LOGINID::20100610>>

DN 92:72789

OREF 92:11953a,11956a

TI Properties of citrate-stimulated starch synthesis catalyzed by starch synthase I of developing maize kernels

AU Boyer, Charles D.; Preiss, Jack

CS Dep. Biochem. Biophys., Univ. California, Davis, CA, 95616, USA

SO Plant Physiology (1979), 64(6), 1039-42

CODEN: PLPHAY; ISSN: 0032-0889

DT Journal

LA English

OSC.G 14 THERE ARE 14 CAPLUS RECORDS THAT CITE THIS RECORD (14 CITINGS)

L8 ANSWER 68 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN

TI Multiple forms of (1 → 4)-α-D-glucan, (1 → 4)-α-D-glucan-6-glycosyl transferase from developing Zea mays L. kernels

AB Two major forms of branching enzyme from developing kernels of maize were detected by DEAE-cellulose chromatog. Branching-enzyme I eluted with the column wash and was unassocd. with starch-synthase activity. Branching-enzyme II was bound to DEAE-cellulose and was coeluted with both primed and unprimed starch-synthase activities. Both fractions were further purified by chromatog. on aminoalkyl-Sepharose columns. Native and subunit mol. wts. were estimated at 70,000-90,000 for both enzymes. Thus both enzymes are primarily monomeric. Branching-enzymes I and II could be distinguished by chromatog. on DEAE-cellulose or 4-aminobutyl-Sepharose, and by disk-gel electrophoresis with activity staining. Branching-enzyme I had a lower ratio of activity (phosphorylase stimulation-amylose branching). The ratio varied from 30-60 as compared to .apprx.300-500 for branching-enzyme II. Likewise, branching-enzyme I had a lower Km value for amylose than branching-enzyme II. Both enzymes could introduce further branches into amylopectin. Combined action of the branching enzymes and rabbit-muscle phosphorylase a resulted in similar patterns of incorporation of D-glucose into the growing α-D-glucan and the synthesis of high-mol-weight polymers. However, the α-D-glucans differed, as shown by spectra of I complexes and average unit-chain length. Branching-enzyme II was separated into 2 fractions (IIa and IIb) by chromatog. on 4-aminobutyl-Sepharose.

AN 1978:165893 HCAPLUS <<LOGINID::20100610>>

DN 88:165893

OREF 88:26105a,26108a

TI Multiple forms of (1 → 4)-α-D-glucan, (1 → 4)-α-D-glucan-6-glycosyl transferase from developing Zea mays L. kernels

AU Boyer, Charles D.; Preiss, Jack

CS Dep. Biochem. Biophys., Univ. California, Davis, CA, USA

SO Carbohydrate Research (1978), 61(1), 321-34

CODEN: CRBRAT; ISSN: 0008-6215

DT Journal

LA English

OSC.G 76 THERE ARE 76 CAPLUS RECORDS THAT CITE THIS RECORD (76 CITINGS)

L8 ANSWER 69 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN

TI Multiple forms of starch branching enzyme of  
maize: evidence for independent genetic control

AB Purification of starch-branching enzymes from kernels of 2 nonlinked mutants of  
maize, sugary and amylose-extender, showed the basis of the 2  
mutations to be associated with the previously identified branching enzymes I  
and IIb, resp. Branching enzyme I from sugary kernels was purified the  
same as nonmutant branching enzyme I, but had an altered pattern of  
activity when amylose was used as substrate. In addition to the typical fall  
in absorbance at high wavelengths (500-700 nm) of the amylose-I complex,  
branching of amylose of sugary branching  
enzyme I caused an increase in absorbance at low wavelengths  
(400-550 nm). Branching enzyme IIb was undetected in exts. of  
amylose-extender kernels, whereas branching enzymes I and IIa appeared  
unaltered. Low unprimed starch synthase activity was also observed in  
DEAE-cellulose fractions of amylose-extender maize, but this  
activity was regenerated by the addition of any branching enzyme.

AN 1978:85042 HCAPLUS <<LOGINID::20100610>>  
DN 88:85042  
OREF 88:13337a,13340a

TI Multiple forms of starch branching enzyme of  
maize: evidence for independent genetic control

AU Boyer, Charles D.; Preiss, Jack  
CS Dep. Biochem. Biophys., Univ. California, Davis, CA, USA  
SO Biochemical and Biophysical Research Communications (1978),  
80(1), 169-75  
CODEN: BBRCA9; ISSN: 0006-291X

DT Journal  
LA English

OSC.G 45 THERE ARE 45 CAPLUS RECORDS THAT CITE THIS RECORD (45 CITINGS)

L8 ANSWER 70 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN

TI Interaction of the amylose-extender and waxy mutants of maize

AB The interaction of the amylose-extender (ae) and waxy (wx) mutants of corn  
was studied by determination of changes in kernel dry weight, endosperm  
starch, and  
apparent amylose (percent) during development of the 16 genotypes  
involving the complete dosage series for the 2 loci. Increasing doses of  
the recessive wx allele from 0 to 3 had no effect on kernel dry weight,  
except when the mutant dose at the ae locus was 3. Similarly, increasing  
doses of the wx allele did not decrease endosperm starch until the mutant  
background dosage at the ae locus was 2 or 3. In contrast, increasing  
doses of the recessive ae allele decreased kernel dry weight and endosperm  
starch, regardless of the gene dosage at the wx locus. Increasing dosage  
at both loci had definite effects on apparent amylose content, although  
single doses of the recessive allele at either locus were not  
significantly different from no recessive alleles. Two or 3 doses of the  
wx allele significantly decreased apparent amylose, while 2 or 3 doses of  
the ae allele significantly increased apparent amylose, regardless of the  
gene dosage at the other locus. Based on these data and other information  
in the literature it is proposed that the gene product of the Ae allele  
controls the quantity of an effector, possibly citrate, which stabilizes a  
branching enzyme-starch synthetase complex.  
Thus, the enzyme complex is necessary for normal amylopectin production

AN 1976:574400 HCAPLUS <<LOGINID::20100610>>  
DN 85:174400  
OREF 85:27869a,27872a

TI Interaction of the amylose-extender and waxy mutants of maize

AU Boyer, C. D.; Garwood, D. L.; Shannon, J. C.  
CS Dep. Hortic., Pennsylvania State Univ., University Park, PA, USA  
SO Journal of Heredity (1976), 67(4), 209-14  
CODEN: JOHEA8; ISSN: 0022-1503

DT Journal  
LA English  
OSC.G 5 THERE ARE 5 CAPLUS RECORDS THAT CITE THIS RECORD (5 CITINGS)

L8 ANSWER 71 OF 71 HCAPLUS COPYRIGHT 2010 ACS on STN  
TI Starch synthetases from Vitis vinifera and Zea mays  
AB ADP glucose:  $\alpha$ -1,4-glucan  $\alpha$ -4-glucosyltransferases (starch synthetases) [9030-10-8] from leaves of V. vnifera and leaves and kernels of Z. mays were chromatographed on DEAE-cellulose columns. ADP glucose:  $\alpha$ -1,4-glucan  $\alpha$ -4-glucosyltransferases (starch synthetases) [9030-10-8] from leaves of V. vinifera and leaves and kernels of Z. mays were chromatographed on DEAE-cellulose columns. One form of the enzyme was present in grape leaves having activity both in the presence and absence of primer. Two forms were present in both leaves and kernels of maize. The second peak of activity in maize leaves and the first peak in maize kernels synthesized a polyglucan in the absence of primer. A peak of branching enzyme (Q-enzyme) [9001-97-2] occurred between the 2 starch synthetase peaks with both tissues. When fractions containing starch synthetase and branching enzyme were added to the first leaf starch synthetase peak, up to 100-fold activation of the unprimed reaction occurred. Branching enzyme did not stimulate the unprimed activity of the first kernel peak and no branching enzyme could be detected in this peak. The unprimed product was a branched polyglucan with mainly  $\alpha$ -1,4-links.

AN 1974:459891 HCAPLUS <<LOGINID::20100610>>  
DN 81:59891  
OREF 81:9535a,9538a  
TI Starch synthetases from Vitis vinifera and Zea mays  
AU Hawker, John S.; Downton, John S.  
CS Div. Hortic. Res., CSIRO, Adelaide, Australia  
SO Phytochemistry (Elsevier) (1974), 13(6), 893-900  
CODEN: PYTCAS; ISSN: 0031-9422

DT Journal  
LA English  
OSC.G 2 THERE ARE 2 CAPLUS RECORDS THAT CITE THIS RECORD (2 CITINGS)

=> d his

(FILE 'HOME' ENTERED AT 13:42:08 ON 10 JUN 2010)

FILE 'HCAPLUS' ENTERED AT 13:42:39 ON 10 JUN 2010

L1 1369 S BRANCHING ENZYME  
L2 44820 S MAIZE  
L3 263 S L1 AND L2  
L4 96 S L3 AND (PY<2000 OR AY<2000 OR PRY<2000)  
L5 808 S (BRANCHING ENZYME) (4A) (STARCH)  
L6 851 S (BRANCHING ENZYME) (4A) (STARCH OR AMYLOSE OR AMYLOPECTIN)  
L7 231 S L2 AND L6  
L8 71 S L7 AND (PY<2000 OR AY<2000 OR PRY<2000)

=> log hold

COST IN U.S. DOLLARS	SINCE FILE	TOTAL
	ENTRY	SESSION
FULL ESTIMATED COST	228.14	228.36
DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS)	SINCE FILE	TOTAL
	ENTRY	SESSION
CA SUBSCRIBER PRICE	-58.65	-58.65

SESSION WILL BE HELD FOR 120 MINUTES  
STN INTERNATIONAL SESSION SUSPENDED AT 13:44:47 ON 10 JUN 2010

Connecting via Winsock to STN

Welcome to STN International! Enter x:X

LOGINID:SSPTAEXO1623

PASSWORD:

\* \* \* \* \* RECONNECTED TO STN INTERNATIONAL \* \* \* \* \*  
SESSION RESUMED IN FILE 'HCAPLUS' AT 14:32:30 ON 10 JUN 2010  
FILE 'HCAPLUS' ENTERED AT 14:32:30 ON 10 JUN 2010  
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COST IN U.S. DOLLARS	SINCE FILE	TOTAL
	ENTRY	SESSION
FULL ESTIMATED COST	228.14	228.36
DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS)	SINCE FILE	TOTAL
	ENTRY	SESSION
CA SUBSCRIBER PRICE	-58.65	-58.65

=> s expression or expressed or (degree of branching) or (branching degree) or  
isolated or isolation or purified

1251007 EXPRESSION  
565632 EXPRESSED  
4754868 DEGREE  
65463 BRANCHING  
2426 DEGREE OF BRANCHING  
(DEGREE(1W)BRANCHING)  
65463 BRANCHING  
4754868 DEGREE  
529 BRANCHING DEGREE  
(BRANCHING(W)DEGREE)  
971851 ISOLATED  
302919 ISOLATION  
479673 PURIFIED  
L9 2911043 EXPRESSION OR EXPRESSED OR (DEGREE OF BRANCHING) OR (BRANCHING  
DEGREE) OR ISOLATED OR ISOLATION OR PURIFIED

=> s 18 and 19

L10 60 L8 AND L9

=> s expression or expressed or (degree of branching) or (branching degree)

1251007 EXPRESSION  
565632 EXPRESSED  
4754868 DEGREE  
65463 BRANCHING  
2426 DEGREE OF BRANCHING  
(DEGREE(1W)BRANCHING)  
65463 BRANCHING  
4754868 DEGREE  
529 BRANCHING DEGREE  
(BRANCHING(W)DEGREE)  
L11 1540936 EXPRESSION OR EXPRESSED OR (DEGREE OF BRANCHING) OR (BRANCHING  
DEGREE)



=> s 18 and 111  
L12 33 L8 AND L11

=> d 112 1-33 ti abs bib

L12 ANSWER 1 OF 33 HCAPLUS COPYRIGHT 2010 ACS on STN

TI Protein and cDNA sequences of corn gene dull1 coding for a starch synthase and use

AB The maize gene dull1 (dul) of the present invention is a determinant of the structure of endosperm starch. Mutations of dul affect the activity of at least two enzymes involved in starch biosynthesis, namely the starch synthase, SSII, and the starch branching enzyme, SBEIIa. Dul codes for a predicted 1674 residue protein, and is expressed with a unique temporal pattern in endosperm but is undetectable in leaf or root. The size of the Dul product and its expression pattern match precisely the known characteristics of maize SSII. The Dul product contains two different repeated regions in its unique amino terminus, one of which is identical to a conserved segment of the starch debranching enzymes. The cDNA provided for in the present invention encodes SSII, and mutations within this gene affect multiple aspects of starch biogenesis by disrupting an enzyme complex containing starch synthase(s), starch branching enzyme(s), and possibly starch debranching enzyme.

AN 2003:851297 HCAPLUS <<LOGINID::20100610>>

DN 139:334824

TI Protein and cDNA sequences of corn gene dull1 coding for a starch synthase and use

IN Myers, Alan M.; James, Martha Graham

PA Iowa State University Research Foundation, Inc., USA

SO U.S., 56 pp., Cont.-in-part of U.S. Ser. No. 968,542.

CODEN: USXXAM

DT Patent

LA English

FAN.CNT 2

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
	-----	---	-----	-----	-----
PI	US 6639125	B1	20031028	US 2000-554467	20000512 <--
	US 5981728	A	19991109	US 1997-968542	19971112 <--
	WO 9924575	A1	19990520	WO 1998-US24225	19981112 <--
	W: AL, AM, AT, AU, AZ, BB, BG, BR, BY, CA, CH, CN, CZ, DE, DK, EE, ES, FI, GB, GE, HU, IL, IS, JP, KE, KG, KP, KR, KZ, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, TJ, TM, TR, TT, UA, UG, US, UZ, VN				
	RW: GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
	US 20040049810	A1	20040311	US 2003-634262	20030805 <--
PRAI	US 1997-968542	A2	19971112	<--	
	WO 1998-US24225	W	19981112	<--	
	US 2000-554467	A1	20000512		

ASSIGNMENT HISTORY FOR US PATENT AVAILABLE IN LSUS DISPLAY FORMAT

OSC.G 1 THERE ARE 1 CAPLUS RECORDS THAT CITE THIS RECORD (1 CITINGS)

RE.CNT 16 THERE ARE 16 CITED REFERENCES AVAILABLE FOR THIS RECORD

ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 2 OF 33 HCAPLUS COPYRIGHT 2010 ACS on STN

TI The rice actin 2 promoter and intron and their use for plant transformation

AB The current invention provides regulatory regions from the rice actin 2

gene. In particular, the current invention provides the rice actin 2 promoter and actin 2 intron. Compns. comprising these sequences are described, as well as transformation constructs derived therefrom. Further provided are methods for the expression of transgenes in plants comprising the use of these sequences. The methods of the invention include the direct creation of transgenic plants with the rice actin 2 intron and/or promoter directly by genetic transformation, as well as by plant breeding methods. The actin 2 sequences of the invention represent a valuable new tool for the creation of transgenic plants, preferably having one or more added beneficial characteristics.

AN 2000:824429 HCAPLUS <<LOGINID::20100610>>

DN 133:359795

TI The rice actin 2 promoter and intron and their use for plant transformation

IN McElroy, David; Wu, Ray

PA Dekalb Genetics Corporation, USA; Cornell Research Foundation, Inc.

SO PCT Int. Appl., 180 pp.

CODEN: PIXXD2

DT Patent

LA English

FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2000070067	A1	20001123	WO 2000-US13303	20000512 <--
	W:			AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW	
	RW:			GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG	
	US 6429357	B1	20020806	US 1999-312304	19990514 <--
	CA 2372859	A1	20001123	CA 2000-2372859	20000512 <--
	EP 1179081	A1	20020213	EP 2000-942636	20000512 <--
	R:			AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO	
	EP 2123764	A1	20091125	EP 2009-169512	20000512 <--
	R:			AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LI, LU, MC, NL, PT, SE	
PRAI	US 1999-312304	A1	19990514	<--	
	EP 2000-942636	A3	20000512		
	WO 2000-US13303	W	20000512		

ASSIGNMENT HISTORY FOR US PATENT AVAILABLE IN LSUS DISPLAY FORMAT

OSC.G 3 THERE ARE 3 CAPLUSRECORDS THAT CITE THIS RECORD (3 CITINGS)

RE.CNT 8 THERE ARE 8 CITED REFERENCES AVAILABLE FOR THIS RECORD

ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 3 OF 33 HCAPLUS COPYRIGHT 2010 ACS on STN

TI Biosynthesis of altered starch in genetically modified plants with glycogen branching enzyme gene

AB A method and compns. for altering starch properties in wheat and maize plants, starch obtained by such method, and transgenic plants producing such starch, are disclosed. Starch with altered properties is produced by introducing a gene construct comprising a glycogen branching enzyme coding sequence under the control of a promoter directing expression and a terminator. A transit peptide for translocation of the glycogen branching enzyme to the plant plastid may also be included in the chimeric gene construct. The starch has altered processing characteristics, in particular an decreased chain length. A chimeric gene containing the High Mol. Weight Glutenin (HMWG) promoter,

nopaline

synthase terminator, and the transit-peptide region of the small-subunit of the ribulose biphosphate carboxylase (ssu of Rubisco) gene was utilized to direct expression of Escherichia coli glycogen branching enzyme (glgB) to wheat and maize. Expression of the glgB gene product in wheat and maize grain was detected by immunoblot anal. Anal. of the starch from these transgenic wheat and maize lines indicated an decrease in chain length, particularly an increase in chain length between 5 and 8 glucose units. The above parameters indicate a novel wheat and maize starch based on expression of the glgB E. coli gene product in transgenic plants.

AN 2000:368616 HCAPLUS <<LOGINID::20100610>>  
 DN 133:29689  
 TI Biosynthesis of altered starch in genetically modified plants with glycogen branching enzyme gene  
 IN Burrell, Michael Meyrick  
 PA Advanced Technologies (Cambridge) Limited, UK  
 SO PCT Int. Appl., 56 pp.  
 CODEN: PIXXD2  
 DT Patent  
 LA English  
 FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2000031282	A1	20000602	WO 1999-GB3762	19991108 <--
	W:	AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, EE, ES, FI, GB, GE, GH, GM, HR, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, UZ, VN, YU, ZA, ZW			
	RW:	GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG			
PRAI	GB 1998-25262	A	19981119	<--	
OSC.G	1	THERE ARE 1 CAPLUS RECORDS THAT CITE THIS RECORD (1 CITINGS)			
RE.CNT	8	THERE ARE 8 CITED REFERENCES AVAILABLE FOR THIS RECORD			
	ALL CITATIONS AVAILABLE IN THE RE FORMAT				

L12 ANSWER 4 OF 33 HCAPLUS COPYRIGHT 2010 ACS on STN

TI Biosynthesis of altered starch in genetically modified plants with glycogen synthase gene

AB A method and compns. for altering starch properties in wheat and maize plants , starch obtained by such method, and transgenic plants producing such starch, are disclosed. Starch with altered properties is produced by introducing a gene construct comprising a glycogen synthase coding sequence under the control of a promoter directing expression and a terminator. A transit peptide for translocation of the glycogen synthase to the plant plastid may also be included in the chimeric gene construct. The starch has altered processing characteristics, in particular an increased chain length. A chimeric gene containing the High Mol. Weight Glutenin (HMWG) promoter, nopaline synthase terminator, and the transit-peptide region of the small-subunit of the ribulose biphosphate carboxylase (ssu of Rubisco) gene was utilized to direct expression of Escherichia coli glycogen synthase (glgA) to wheat and maize. Expression of the glgA gene product in wheat and maize grain was detected by immunoblot anal. Anal. of the starch from these transgenic wheat and maize lines indicated an increase in chain length, particularly in chain length between 17 and 28 glucose units. Rapid viscometric anal. yielded lower peak and final viscosity values (about 30% of control values), whereas differential scanning calorimetry values indicated

increased enthalpy values. The above parameters indicate a novel wheat and maize starch based on expression of the glgA E. coli gene product in transgenic plants.

AN 2000:368603 HCAPLUS <<LOGINID::20100610>>  
 DN 133:29688  
 TI Biosynthesis of altered starch in genetically modified plants with glycogen synthase gene  
 IN Burrell, Michael Meyrick  
 PA Advanced Technologies (Cambridge) Limited, UK  
 SO PCT Int. Appl., 66 pp.  
 CODEN: PIXXD2  
 DT Patent  
 LA English  
 FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2000031274	A1	20000602	WO 1999-GB3734	19991109 <--
	W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, EE, ES, FI, GB, GE, GH, GM, HR, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, UZ, VN, YU, ZA, ZW				
	RW: GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
	CA 2349819	A1	20000602	CA 1999-2349819	19991109 <--
	CA 2349819	C	20080909		
	EP 1131442	A1	20010912	EP 1999-954197	19991109 <--
	EP 1131442	B1	20100526		
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, CY				
	US 6468799	B1	20021022	US 1999-444728	19991118 <--
	AU 2000010616	A	20000807	AU 2000-10616	20000119 <--
	AU 2004202150	A1	20040617	AU 2004-202150	20040519
	AU 2004202150	B2	20060713		
PRAI	GB 1998-25242	A	19981119	<--	
	WO 1999-GB3734	W	19991109	<--	
	AU 2000-10616	A3	20000119		

ASSIGNMENT HISTORY FOR US PATENT AVAILABLE IN LSUS DISPLAY FORMAT  
 OSC.G 2 THERE ARE 2 CAPLUS RECORDS THAT CITE THIS RECORD (2 CITINGS)  
 RE.CNT 7 THERE ARE 7 CITED REFERENCES AVAILABLE FOR THIS RECORD  
 ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 5 OF 33 HCAPLUS COPYRIGHT 2010 ACS on STN  
 TI Starch branching enzyme II (SBEII-1 and SBEII-2) isoforms from wheat, cDNA, transgenic plants, and altering starch properties for food use  
 AB A class of wheat SBEII genes, SBEII-1, recombinant protein expression in transgenic plants, and its use in altering properties of starch produced by a plant are claimed. Starch properties include the gelatinization onset and/or peak temperature The use of such starch with altered properties in food stuff, particularly bakery products is also claimed. CDNA clones for SBEII were isolated and sequenced. Those clones were divided into two sub-classes, SBEII-1 and SBEII-2 having sequence homol. to maize SBEIIb and SBEIIa, resp. These genes were mapped to the long arm of wheat group 2 homologous chromosomes. Some of those isoforms were expressed as recombinant protein in wheat. Differential scanning calorimetry studies showed that starch produced in transgenic wheat transformed with expression construct for SBEII displayed higher onset, peak, and end temperature for

gelatinization.  
AN 2000:191230 HCAPLUS <<LOGINID::20100610>>  
DN 132:247996  
TI Starch branching enzyme II (SBEII-1 and  
SBEII-2) isoforms from wheat, cDNA, transgenic plants, and altering starch  
properties for food use  
IN Goldsbrough, Andrew; Colliver, Steve  
PA Plant Breeding International Cambridge Ltd., UK  
SO PCT Int. Appl., 198 pp.  
CODEN: PIXXD2  
DT Patent  
LA English  
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2000015810	A1	20000323	WO 1999-GB3011	19990909 <--
	W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZA, ZW				
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	AU 9958725	A	20000403	AU 1999-58725	19990909 <--
	AU 767103	B2	20031030		
	EP 1117814	A1	20010725	EP 1999-946307	19990909 <--
	EP 1117814	B1	20100217		
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, CY				
	HU 2001003618	A2	20020128	HU 2001-3618	19990909 <--
	HU 2001003618	A3	20031229		
	AT 458061	T	20100315	AT 1999-946307	19990909 <--
	US 6730825	B1	20040504	US 2001-786480	20010917 <--
	US 20040216188	A1	20041028	US 2004-818770	20040406 <--
	US 7217857	B2	20070515		
	US 20080064864	A1	20080313	US 2007-788837	20070419 <--
	US 7465851	B2	20081216		
PRAI	EP 1998-307337	A	19980910	<--	
	WO 1999-GB3011	W	19990909	<--	
	US 2001-786480	A3	20010917		
	US 2004-818770	A3	20040406		

ASSIGNMENT HISTORY FOR US PATENT AVAILABLE IN LSUS DISPLAY FORMAT  
OSC.G 3 THERE ARE 3 CAPLUS RECORDS THAT CITE THIS RECORD (3 CITINGS)  
RE.CNT 4 THERE ARE 4 CITED REFERENCES AVAILABLE FOR THIS RECORD  
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 6 OF 33 HCAPLUS COPYRIGHT 2010 ACS on STN  
TI Expression control elements from the 5'- and 3'-regions of genes  
for starch branching enzymes  
AB Regulatory elements from the 5'- and 3'-flanking regions of maize  
genes for starch branching enzymes (SbeI and Ae) are described for use in  
the expression of foreign genes in transgenic plants. The genes  
show different patterns of expression in tissues of the seed  
during its development and so the regulatory elements may be of use in the  
regulation of foreign gene expression in cereals. The genes  
were cloned by screening a genomic library with PCR products. The SbeI  
gene has a perfectly palindromic G-box in the promoter region while the Ae  
gene had elements resembling metal responsive elements, GC boxes, Hex, and  
I boxes. Functional anal. of the SbeI promoter identified sequences  
responsible for high level transcription and sugar regulation of gene

expression. It also showed that elements within the transcribed region play a role in high level gene expression and that there sequences in the 5'-region that limit gene expression. An essential region of 60 bp was identified and shown to bind DNA-binding proteins.

AN 1999:795936 HCAPLUS <<LOGINID::20100610>>

DN 132:31802

TI Expression control elements from the 5'- and 3'-regions of genes for starch branching enzymes

IN Guiltinan, Mark J.; Kim, Kyung-Nam

PA The Pennsylvania State University, USA

SO PCT Int. Appl., 110 pp.

CODEN: PIXXD2

DT Patent

LA English

FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
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PI	WO 9964562	A2	19991216	WO 1999-US13266	19990611 <--
	WO 9964562	A3	20000518		
	W:	AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, UZ, VN, YU, ZA, ZW			
	RW:	GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG			
	AU 9944384	A	19991230	AU 1999-44384	19990611 <--
PRAI	US 1998-89049P	P	19980612	<--	
	US 1998-89050P	P	19980612	<--	
	WO 1999-US13266	W	19990611	<--	

RE.CNT 2 THERE ARE 2 CITED REFERENCES AVAILABLE FOR THIS RECORD

ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 7 OF 33 HCAPLUS COPYRIGHT 2010 ACS on STN

TI Carbon isotope ratios of amylose, amylopectin and mutant starches

AB Carbon isotope ratios (expressed as  $\delta^{13}\text{C}$  values) were determined for various sources of starch and the starch fractions amylose and amylopectin. The  $\delta^{13}\text{C}$  values of amylose were consistently less neg., 0.4-2.3.permill., than those of amylopectin in kernel starch from maize (*Zea mays*) and barley (*Hordeum vulgare*) and in tuber starch from potato (*Solanum tuberosum*). Kernel starch isolated from the maize mutants wx1 and ael, with known genetic lesions in the starch biosynthetic pathway, also showed significant differences in  $\delta^{13}\text{C}$  values. Collectively, these results suggest that variation in carbon isotope ratios in the amylose and amylopectin components of starch may be attributed to isotopic discrimination by the enzymes involved in starch biosynthesis.

AN 1999:737017 HCAPLUS <<LOGINID::20100610>>

DN 132:76065

TI Carbon isotope ratios of amylose, amylopectin and mutant starches

AU Scott, M. Paul; Jane, Jay-Lin; Soundararajan, Madhavan

CS USDA-ARS, Department of Agronomy, Iowa State University, Ames, IA, 50011, USA

SO Phytochemistry (1999), 52(4), 555-559

CODEN: PYTCAS; ISSN: 0031-9422

PB Elsevier Science Ltd.

DT Journal

LA English

OSC.G 3 THERE ARE 3 CAPLUS RECORDS THAT CITE THIS RECORD (3 CITINGS)

RE.CNT 24 THERE ARE 24 CITED REFERENCES AVAILABLE FOR THIS RECORD  
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 8 OF 33 HCAPLUS COPYRIGHT 2010 ACS on STN

TI Expression of transgenes in plants using promoter and terminator sequences from Coix

AB Methods and compns. for the expression of transgenes in monocot plants including maize are disclosed. In the invention, gene silencing is avoided by use of monocot-homeologous sequences from plants of the genus Coix for transformation. Included in these transgene sequences are Coix promoters, enhancers, coding sequences and terminators. Suitable alternatives to maize-derived transgenes are desirable for expression in maize in that homol.-based gene silencing can limit or effectively eliminate transgene expression

AN 1999:736897 HCAPLUS <<LOGINID::20100610>>

DN 131:347500

TI Expression of transgenes in plants using promoter and terminator sequences from Coix

IN Kriz, Alan L.; Luethy, Michael H.; Voyles, Dale A.

PA Dekalb Genetics Corporation, USA

SO PCT Int. Appl., 240 pp.

CODEN: PIXXD2

DT Patent

LA English

FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 9958659	A2	19991118	WO 1999-US10776	19990514 <--
	WO 9958659	A3	20000120		
	W:	AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZA, ZW			
	RW:	GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG			
	US 6635806	B1	20031021	US 1998-78972	19980514 <--
	CA 2328129	A1	19991118	CA 1999-2328129	19990514 <--
	AU 9939957	A	19991129	AU 1999-39957	19990514 <--
	EP 1076706	A2	20010221	EP 1999-923112	19990514 <--
	EP 1076706	B1	20080206		
	R:	AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI, CY			
	TR 2001000104	T2	20010621	TR 2001-104	19990514 <--
	BR 9910455	A	20011127	BR 1999-10455	19990514 <--
	JP 2002533057	T	20021008	JP 2000-548450	19990514 <--
	AT 385518	T	20080215	AT 1999-923112	19990514 <--
	PT 1076706	E	20080509	PT 1999-923112	19990514 <--
	ES 2301239	T3	20080616	ES 1999-923112	19990514 <--
	IN 2000DN00321	A	20080620	IN 2000-DN321	20001109 <--
	IN 227562	A1	20090130		
	ZA 2000006576	A	20020213	ZA 2000-6576	20001113 <--
	MX 2000011199	A	20010419	MX 2000-11199	20001114 <--
	US 20050250938	A1	20051110	US 2003-660097	20030911 <--
	US 7256283	B2	20070814		
	IN 2005DN05625	A	20070928	IN 2005-DN5625	20051205 <--
	US 20080271212	A1	20081030	US 2007-838724	20070814 <--
	US 20090013423	A1	20090108	US 2007-838725	20070814 <--
	US 20090199307	A1	20090806	US 2007-838721	20070814 <--

PRAI US 1998-78972            A1       19980514 <--  
WO 1999-US10776            W       19990514 <--  
IN 2000-DN321            A3       20001109  
US 2003-660097            A3       20030911

ASSIGNMENT HISTORY FOR US PATENT AVAILABLE IN LSUS DISPLAY FORMAT

OSC.G    5        THERE ARE 5 CAPLUS RECORDS THAT CITE THIS RECORD (8 CITINGS)  
RE.CNT   1        THERE ARE 1 CITED REFERENCES AVAILABLE FOR THIS RECORD  
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 9 OF 33 HCAPLUS COPYRIGHT 2010 ACS on STN

TI Identification of cis-acting elements important for expression  
of the starch-branching enzyme I gene in  
maize endosperm

AB The genes encoding the starch-branching enzymes (SBE) SBEI, SBEIIa, and  
SBEIIb in maize (Zea mays) are differentially regulated in  
tissue specificity and during kernel development. To gain insight into  
the regulatory mechanisms controlling their expression, we  
analyzed the 5'-flanking sequences of SbeI using a transient gene  
expression system. Although the 2.2-kb 5'-flanking sequence  
between -2,190 and +27 relative to the transcription initiation site was  
sufficient to promote transcription, the addition of the transcribed region  
between +28 and +228 containing the first exon and intron resulted in  
high-level expression in suspension-cultured maize  
endosperm cells. A series of 5' deletion and linker-substitution mutants  
identified two critical pos. cis elements, -314 to -295 and -284 to -255. An  
electrophoretic mobility-shift assay showed that nuclear proteins prepared  
from maize kernels interact with the 60-bp fragment containing these  
two elements. Expression of the SbeI gene is regulated by sugar  
concentration in suspension-cultured maize endosperm cells, and the  
region -314 to -145 is essential for this effect. Interestingly, the  
expression of mEmBP-1, a bZIP transcription activator, in  
suspension-cultured maize endosperm cells resulted in a 5-fold  
decrease in SbeI promoter activity, suggesting a possible regulatory role  
of the G-box present in the SbeI promoter from -227 to -220.

AN 1999:615638 HCAPLUS <<LOGINID::20100610>>

DN 132:815

TI Identification of cis-acting elements important for expression  
of the starch-branching enzyme I gene in  
maize endosperm

AU Kim, Kyung-Nam; Guiltinan, Mark J.

CS Intercollege Graduate Program in Plant Physiology, The Biotechnology  
Institute, and Department of Horticulture, The Pennsylvania State  
University, University Park, PA, 16802, USA

SO Plant Physiology (1999), 121(1), 225-236

CODEN: PLPHAY; ISSN: 0032-0889

PB American Society of Plant Physiologists

DT Journal

LA English

OSC.G    17        THERE ARE 17 CAPLUS RECORDS THAT CITE THIS RECORD (17 CITINGS)

RE.CNT   65        THERE ARE 65 CITED REFERENCES AVAILABLE FOR THIS RECORD

ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 10 OF 33 HCAPLUS COPYRIGHT 2010 ACS on STN

TI Maize starch synthase gene dul and uses in starch production

AB Disclosed are the maize dul gene, the encoded starch synthase  
isoenzyme II, and production of starch with recombinant dul-expressing cells  
or transgenic plants. The maize gene dull1 (dul) of the present  
invention is a determinant of the structure of endosperm starch.  
Mutations of dul affect the activity of at least two enzymes involved in  
starch biosynthesis, namely the starch synthase, SSII, and the  
starch branching enzyme, SBEIIa. Dul codes



for a predicted 1674 residue protein, and is expressed with a unique temporal pattern in endosperm but is undetectable in leaf or root. The size of the Dul product and its expression pattern match precisely the known characteristics of maize SSII. The Dul product contains two different repeated regions in its unique amino terminus, one of which is identical to a conserved segment of the starch debranching enzymes. The cDNA provided for in the present invention encodes SSII, and mutations within this gene affect multiple aspects of starch biogenesis by disrupting an enzyme complex containing starch synthase(s), starch branching enzyme(s), and possibly starch debranching enzyme(s).

AN 1999:326050 HCAPLUS <<LOGINID::20100610>>  
 DN 130:333760  
 TI Maize starch synthase gene dul and uses in starch production  
 IN Myers, Alan M.; James, Martha G.  
 PA Iowa State University Research Foundation, Inc., USA  
 SO PCT Int. Appl., 138 pp.  
 CODEN: PIXXD2  
 DT Patent  
 LA English  
 FAN.CNT 2

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 9924575	A1	19990520	WO 1998-US24225	19981112 <--
	W: AL, AM, AT, AU, AZ, BB, BG, BR, BY, CA, CH, CN, CZ, DE, DK, EE, ES, FI, GB, GE, HU, IL, IS, JP, KE, KG, KP, KR, KZ, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, TJ, TM, TR, TT, UA, UG, US, UZ, VN				
	RW: GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
	US 5981728	A	19991109	US 1997-968542	19971112 <--
	CA 2309346	A1	19990520	CA 1998-2309346	19981112 <--
	AU 9915236	A	19990531	AU 1999-15236	19981112 <--
	AU 761419	B2	20030605		
	EP 1030922	A1	20000830	EP 1998-959440	19981112 <--
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
	BR 9814864	A	20011106	BR 1998-14864	19981112 <--
	JP 2001522604	T	20011120	JP 2000-520569	19981112 <--
	NZ 504534	A	20021220	NZ 1998-504534	19981112 <--
	MX 2000004586	A	20001110	MX 2000-4586	20000512 <--
	US 6639125	B1	20031028	US 2000-554467	20000512 <--
PRAI	US 1997-968542	A	19971112	<--	
	WO 1998-US24225	W	19981112	<--	

ASSIGNMENT HISTORY FOR US PATENT AVAILABLE IN LSUS DISPLAY FORMAT

OSC.G 1 THERE ARE 1 CAPLUS RECORDS THAT CITE THIS RECORD (1 CITINGS)

RE.CNT 1 THERE ARE 1 CITED REFERENCES AVAILABLE FOR THIS RECORD  
 ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 11 OF 33 HCAPLUS COPYRIGHT 2010 ACS on STN

TI Characterization of a gene encoding wheat endosperm starch branching enzyme-I

AB A genomic DNA fragment from *Triticum tauschii*, the donor of the wheat D genome, contains a starch branching enzyme-I (SBE-I) gene spread over 6.5 kb. This gene (designated wSBE I-D4) encodes an amino acid sequence identical to that determined for the N-terminus of SBE-I from the hexaploid wheat (*T. aestivum*) endosperm. Cognate cDNA sequences for wSBE I-D4 were isolated from hexaploid wheat by hybridization screening from an endosperm library and also by PCR. A contiguous sequence (D4 cDNA) was assembled from the sequence of five overlapping

partial cDNAs which spanned wSBE I-D4. D4 cDNA encodes a mature polypeptide of 87 kDa that shows 90% identity to SBE-I amino acid sequences from rice and maize and contains all the residues considered essential for activity. D4 mRNA has been detected only in the endosperm and is at a maximum concentration mid-way through grain development.

The

wSBE I-D4 gene consists of 14 exons, similar to the structure for the equivalent gene in rice; the rice gene has a strikingly longer intron 2. The 3' end of wSBE I-D4 was used to show that the gene is located on group 7 chromosomes. The sequence upstream of wSBE I-D4 was analyzed with respect to conserved motifs.

AN 1999:177589 HCAPLUS <<LOGINID::20100610>>

DN 131:83671

TI Characterization of a gene encoding wheat endosperm starch branching enzyme-I

AU Rahman, S.; Li, Z.; Abrahams, S.; Abbott, D.; Appels, R.; Morell, M. K.

CS CSIRO Plant Industry, Canberra, 2601, Australia

SO Theoretical and Applied Genetics (1999), 98(1), 156-163

CODEN: THAGA6; ISSN: 0040-5752

PB Springer-Verlag

DT Journal

LA English

OSC.G 24 THERE ARE 24 CAPLUS RECORDS THAT CITE THIS RECORD (24 CITINGS)

RE.CNT 32 THERE ARE 32 CITED REFERENCES AVAILABLE FOR THIS RECORD

ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 12 OF 33 HCAPLUS COPYRIGHT 2010 ACS on STN

TI Molecular cloning and characterization of the Amylose-Extender gene encoding starch branching enzyme IIB in maize

AB The amylose-extender (Ae) gene encoding starch-branching enzyme IIB (SBEIIB) in maize is predominantly expressed in endosperm and embryos during kernel development. A maize genomic DNA fragment (-2964 to +20485) containing the Ae gene was isolated and sequenced. The maize Ae mRNA is derived from 22 exons distributed over 16914 bp. Twenty-one introns, differing in length from 76 bp to 4020 bp, all have conserved junction sequences (GT••AG). Sequence anal. of the 5'- and 3'-flanking regions revealed a consensus TATA-box sequence located 28 bp upstream of the transcription initiation site as determined by primer extension anal., and a putative polyadenylation signal observed 29 bp upstream of the polyadenylation site based on cDNA sequence. Genomic Southern blot anal. suggests that a single Ae gene is present in the maize genome. Promoter activity was confirmed by testing a transcriptional fusion of the Ae 5'-flanking region between -2964 and +100 to a luciferase reporter gene in a transient expression assay using maize endosperm suspension cultured cells. 5' deletion anal. revealed that the 111 bp region from -160 to -50 is essential for high-level promoter activity.

AN 1999:44300 HCAPLUS <<LOGINID::20100610>>

DN 130:219005

TI Molecular cloning and characterization of the Amylose-Extender gene encoding starch branching enzyme IIB in maize

AU Kim, Kyung-Nam; Fisher, Dane K.; Gao, Ming; Guiltinan, Mark J.

CS Intercollege Graduate Programs in Plant Physiology and Genetics, The Biotechnology Institute, and Department of Horticulture, The Pennsylvania State University, University Park, PA, 16802, USA

SO Plant Molecular Biology (1998), 38(6), 945-956

CODEN: PMBIDB; ISSN: 0167-4412

PB Kluwer Academic Publishers

DT Journal

LA English

OSC.G 26 THERE ARE 26 CAPLUS RECORDS THAT CITE THIS RECORD (26 CITINGS)

RE.CNT 55 THERE ARE 55 CITED REFERENCES AVAILABLE FOR THIS RECORD  
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 13 OF 33 HCAPLUS COPYRIGHT 2010 ACS on STN

TI Manipulating the starch composition of potato

AB A review with 41 refs. Starch can be fractionated into two types of glucose polymers: amylose and amylopectin. Amylose consists of essentially linear chains of  $\alpha$ -(1,4)-linked glucose residues, whereas amylopectin is built up from  $\alpha$ -(1,4)-linked chains with  $\alpha$ -(1,6)-linked branches. The composition and fine structure of starch are responsible for many of the physicochem. properties and thus det. its industrial uses. Variation in starch structure and composition can be found between and within crops. In the latter case it can be found in mutants, often resulting from the loss of function of one or more of the genes involved in starch biosynthesis. In maize, the most extensively studied crop, mutant genotypes are known for nearly every gene identified as being involved in starch biosynthesis. Differences in starch composition can also be achieved by genetic modifications such as antisense inhibition of genes or overexpression of (heterologous) genes. Most examples of genetic modification of starch composition are in potato, which can easily be transformed. Antisense inhibition of enzymes in the biosynthetic pathway, such as ADP glucose phosphorylase (AGP), (granule-bound) starch synthase or branching enzyme, lead to an altered starch content and/or composition. In addition, the introduction and expression of bacterial genes, such as genes of the Escherichia coli glycogen synthesis pathway, in potato leads to starches with altered content, composition, structure and physicochem. properties. Studying the physicochem. properties of these altered starches will, together with the information obtained by research on starches of mutants, help to clarify the precise relationship between structural and functional features of starch.

AN 1998:787972 HCAPLUS <<LOGINID::20100610>>

DN 130:165463

TI Manipulating the starch composition of potato

AU Kortstee, A. J.; Flipse, E.; Kuipers, A. G. J.; Jacobsen, E.; Visser, R. G. F.

CS Graduate School of Experimental Plant Sciences, Department of Plant Breeding, Agricultural University Wageningen, Wageningen, 6700 AJ, Neth.

SO Portland Press Proceedings (1998), 14(Engineering Crop Plants for Industrial End Uses), 89-98  
CODEN: POPPEF; ISSN: 0966-4068

PB Portland Press Ltd.

DT Journal; General Review

LA English

OSC.G 1 THERE ARE 1 CAPLUS RECORDS THAT CITE THIS RECORD (1 CITINGS)

RE.CNT 41 THERE ARE 41 CITED REFERENCES AVAILABLE FOR THIS RECORD  
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 14 OF 33 HCAPLUS COPYRIGHT 2010 ACS on STN

TI Analysis of essential histidine residues of maize branching enzymes by chemical modification and site-directed mutagenesis

AB Incubation of maize branching enzyme, mBEI and mBEII, with 100  $\mu$ M diethylpyrocarbonate (DEPC) rapidly inactivated the enzymes. Treatment of the DEPC-inactivated enzymes with 100-500 mM hydroxylamine restored the enzyme activities. Spectroscopic data indicated that the inactivation of BE with DEPC was the result of histidine modification. The addition of the substrate amylose or amylopectin retarded the enzyme inactivation by DEPC, suggesting that the histidine residues are important for substrate binding. In maize BEII, conserved histidine

residues are in catalytic regions 1 (His320) and 4 (His508). His320 and His508 were individually replaced by Ala via site-directed mutagenesis to probe their role in catalysis. Expression of these mutants in *E. coli* showed a significant decrease of the activity and the mutant enzymes had  $K_m$  values 10 times higher than the wild type. Therefore, residues His320 and His508 do play an important role in substrate binding.

AN 1998:784558 HCAPLUS <<LOGINID::20100610>>

DN 130:121357

TI Analysis of essential histidine residues of maize branching enzymes by chemical modification and site-directed mutagenesis

AU Funane, Kazumi; Libessart, Nathalie; Stewart, Douglas; Michishita, Toru; Preiss, Jack

CS Department of Biochemistry, Michigan State University, East Lansing, MI, 48824, USA

SO Journal of Protein Chemistry (1998), 17(7), 579-590

CODEN: JPCHD2; ISSN: 0277-8033

PB Plenum Publishing Corp.

DT Journal

LA English

OSC.G 10 THERE ARE 10 CAPLUS RECORDS THAT CITE THIS RECORD (10 CITINGS)

RE.CNT 54 THERE ARE 54 CITED REFERENCES AVAILABLE FOR THIS RECORD

ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 15 OF 33 HCAPLUS COPYRIGHT 2010 ACS on STN

TI Genomic organization and promoter activity of the maize starch branching enzyme I gene

AB Starch branching enzymes (SBE) which catalyze the formation of  $\alpha$ -1,6-glucan linkages are of crucial importance for the quantity and quality of starch synthesized in plants. In maize (*Zea mays* L.), three SBE isoforms (SBEI, IIa and IIb) have been identified and shown to exhibit differential expression patterns. As a first step toward understanding the regulatory mechanisms controlling their expression, the authors isolated and sequenced a maize genomic DNA (-2190 to +5929) which contains the entire coding region of SBEI (Sbe1) as well as 5'- and 3'-flanking sequences. Using this clone, the authors established a complete genomic organization of the maize Sbe1 gene. The transcribed region consists of 14 exons and 13 introns, distributed over 5.7 kb. A consensus TATA-box and a G-box containing a perfect palindromic sequence, CCACGTGG, were found in the 5'-flanking region. Genomic Southern blot anal. indicated that two Sbe1 genes with divergent 5'-flanking sequences exist in the maize genome, suggesting the possibility that they are differentially regulated. A chimeric construct containing the 5'-flanking region of Sbe1 (-2190 to +27) fused to the  $\beta$ -glucuronidase gene (pKG101) showed promoter activity after it was introduced into maize endosperm suspension cells by particle bombardment.

AN 1998:597027 HCAPLUS <<LOGINID::20100610>>

DN 129:311547

OREF 129:63465a,63468a

TI Genomic organization and promoter activity of the maize starch branching enzyme I gene

AU Kim, Kyung-Nam; Fisher, Dane K.; Gao, Ming; Guiltinan, Mark J.

CS Intercollege Graduate Programs in Plant Physiology and Genetics, Biotechnology Institute, Dep. Horticulture, Pennsylvania State University, Pennsylvania, PA, 16802, USA

SO Gene (1998), 216(2), 233-243

CODEN: GENED6; ISSN: 0378-1119

PB Elsevier Science B.V.

DT Journal

LA English

OSC.G 13 THERE ARE 13 CAPLUS RECORDS THAT CITE THIS RECORD (13 CITINGS)

RE.CNT 42        THERE ARE 42 CITED REFERENCES AVAILABLE FOR THIS RECORD  
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 16 OF 33 HCAPLUS COPYRIGHT 2010 ACS on STN  
TI Altering starch structure and functionality by manipulating  
expression of starch biosynthetic enzymes.  
AB Starch functionality is a product of the fine structure of a given starch  
polymer. This structure is a result of the concerted action of several  
starch synthases, starch branching enzymes and starch debranching enzymes.  
To examine the relationship between starch polymer structure and starch  
functionality we are using transgenic approaches to control the  
expression of genes encoding starch biosynthetic enzymes and  
examine the impacts of altered gene expression on starch  
structure and functionality. We have isoalted and characterized  
maize cDNAs encoding Starch Branching Enzymes I and Ilb (SBE I  
SBEIlb) and generated transgenic maize plants carrying  
constructions for under and over expression of these two genes.  
The effects of altered branching enzyme  
expression on starch polymer structure and starch  
functionality will be presented.  
AN 1998:530122 HCAPLUS <<LOGINID::20100610>>  
TI Altering starch structure and functionality by manipulating  
expression of starch biosynthetic enzymes.  
AU Lightner, Jonathan; Broglie, Karen; Cressman, Robert; Hines, Chris;  
Pearlstein, Rich; Hubbard, Natalie  
CS Stine-Haskell Research Center, DuPont Agricultural Products, Newark, DE,  
19714-0030, USA  
SO Book of Abstracts, 216th ACS National Meeting, Boston, August 23-27 (  
1998), AGFD-137 Publisher: American Chemical Society, Washington,  
D. C.  
CODEN: 66KYA2  
DT Conference; Meeting Abstract  
LA English  
  
L12 ANSWER 17 OF 33 HCAPLUS COPYRIGHT 2010 ACS on STN  
TI Starch granule-associated protein and transgenic plants producing starch  
with altered viscosity and phosphate content  
AB Nucleic acid mols. are described encoding a starch granule-bound protein  
from potato and maize as well as methods and recombinant DNA  
mols. for the production of transgenic plant cells and plants synthesizing a  
modified starch. Potato and maize cDNAs for a starch  
granule-associated protein were cloned and sequenced. Transgenic potatoes  
expressing an antisense version of the potato cDNA produced starch with  
.apprx.50% lower phosphate content and with altered gelling properties.  
When the starch granule-associated protein cDNA was expressed in  
Escherichia coli, glycogen with higher than normal phosphate content was  
produced.  
AN 1998:424347 HCAPLUS <<LOGINID::20100610>>  
DN 129:91420  
OREF 129:18743a,18746a  
TI Starch granule-associated protein and transgenic plants producing starch  
with altered viscosity and phosphate content  
IN Kossmann, Jens; Emmermann, Michael  
PA Planttec Biotechnologie G.m.b.H., Germany  
SO PCT Int. Appl., 123 pp.  
CODEN: PIXXD2  
DT Patent  
LA English  
FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
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PI WO 9827212 A1 19980625 WO 1997-EP7123 19971218 <--  
W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE,  
DK, EE, ES, FI, GB, GE, GH, GM, GW, HU, ID, IL, IS, JP, KE, KG,  
KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX,  
NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT,  
UA, UG, US, UZ, VN, YU, ZW  
RW: GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, DE, DK, ES, FI,  
FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM,  
GA, GN, ML, MR, NE, SN, TD, TG  
DE 19653176 A1 19980625 DE 1996-19653176 19961219 <--  
CA 2272844 A1 19980625 CA 1997-2272844 19971218 <--  
AU 9858577 A 19980715 AU 1998-58577 19971218 <--  
AU 740492 B2 20011108  
EP 950107 A1 19991020 EP 1997-954424 19971218 <--  
EP 950107 B1 20070321  
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, NL, SE, PT  
JP 2001522223 T 20011113 JP 1998-527334 19971218 <--  
JP 4098365 B2 20080611  
AT 357522 T 20070415 AT 1997-954424 19971218 <--  
PT 950107 E 20070531 PT 1997-954424 19971218 <--  
ES 2280086 T3 20070901 ES 1997-954424 19971218 <--  
US 7186898 B1 20070306 US 1999-334103 19990616 <--  
PRAI DE 1996-19653176 A 19961219 <--  
WO 1997-EP7123 W 19971218 <--

ASSIGNMENT HISTORY FOR US PATENT AVAILABLE IN LSUS DISPLAY FORMAT

OSC.G 9 THERE ARE 9 CAPLUS RECORDS THAT CITE THIS RECORD (9 CITINGS)  
RE.CNT 4 THERE ARE 4 CITED REFERENCES AVAILABLE FOR THIS RECORD  
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 18 OF 33 HCAPLUS COPYRIGHT 2010 ACS on STN

TI Promoter of wheat wbeI gene for expressing foreign genes in  
monocotyledonous plants

AB A DNA fragment for directing the expression of foreign or  
endogenous genes or RNA in cells of monocot plants. The fragment  
comprises a sequence corresponding to a first part of a putative type I  
starch branching enzyme gene (wbeI) present in  
wheat and a 5'-region upstream of the gene, or a part of the sequence that  
is effective for increasing the expression of the foreign or  
endogenous gene in the plant cells. The indicated sequence contains two  
promoter regions, P1 and P2. A DNA fragment effective to increase  
expression comprises at least one of the promoter regions, or an  
effective part. The fragment can be obtained from a genomic library of  
wheat and can be fused to suitable genes and markers and inserted into  
suitable vectors for expression in transgenic monocot plants.  
The P2 promoter, found in the second intron, was 2-4 times more active in  
wheat, barley, oat and maize cells that the P1-P2 combination.

AN 1998:256690 HCAPLUS <<LOGINID::20100610>>

DN 128:253799

OREF 128:50155a,50158a

TI Promoter of wheat wbeI gene for expressing foreign genes in  
monocotyledonous plants

IN Baga, Monica; Chibbar, Ravindra N.; Kartha, Kutty K.

PA Baga, Monica, Can.; Chibbar, Ravindra N.; Kartha, Kutty K.

SO Can. Pat. Appl., 78 pp.

CODEN: CPXXEB

DT Patent

LA English

FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	CA 2196834	A1	19971204	CA 1997-2196834	19970205 <--

US 5866793 A 19990202 US 1996-773251 19961223 <--  
PRAI CA 1996-2178016 A 19960603 <--  
ASSIGNMENT HISTORY FOR US PATENT AVAILABLE IN LSUS DISPLAY FORMAT  
OSC.G 5 THERE ARE 5 CAPLUS RECORDS THAT CITE THIS RECORD (5 CITINGS)

L12 ANSWER 19 OF 33 HCAPLUS COPYRIGHT 2010 ACS on STN  
TI Characterization of dull1, a maize gene coding for a novel  
starch synthase  
AB The maize dull1 (dul) gene is a determinant of the structure of  
endosperm starch, and dul-mutations affect the activity of two enzymes  
involved in starch biosynthesis, starch synthase II (SSII) and  
starch branching enzyme IIa (SBEIIa). Six  
novel dul-mutations generated in Mutator-active plants were identified. A  
portion of the dul locus was cloned by transposon tagging, and a nearly  
full-length Dul cDNA sequence was determined Dul codes for a predicted  
1674-residue protein, comprising one portion that is similar to SSIII of  
potato, as well as a large unique region. Dul transcripts are present in  
the endosperm during the time of starch biosynthesis, but the mRNA was  
undetectable in leaf or root tissue. The predicted size of the Dul gene  
product and its expression pattern are consistent with those of  
maize SSII. The Dul gene product contains two repeated regions in  
its unique N terminus. One of these contains a sequence identical to a  
conserved segment of SBEs. We conclude that Dul codes for a starch  
synthase, most likely SSII, and that secondary effects of dul-mutations,  
such as reduction of SBEIIa, result from the primary deficiency in this starch  
synthase.  
AN 1998:215485 HCAPLUS <<LOGINID::20100610>>  
DN 129:2125  
OREF 129:531a,534a  
TI Characterization of dull1, a maize gene coding for a novel  
starch synthase  
AU Gao, Ming; Wanat, Jennifer; Stinard, Philip S.; James, Martha G.; Myers,  
Alan M.  
CS Department of Biochemistry and Biophysics, Iowa State University, Ames,  
IA, 50011, USA  
SO Plant Cell (1998), 10(3), 399-412  
CODEN: PLCEEW; ISSN: 1040-4651  
PB American Society of Plant Physiologists  
DT Journal  
LA English  
OSC.G 100 THERE ARE 100 CAPLUS RECORDS THAT CITE THIS RECORD (100 CITINGS)  
RE.CNT 56 THERE ARE 56 CITED REFERENCES AVAILABLE FOR THIS RECORD  
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 20 OF 33 HCAPLUS COPYRIGHT 2010 ACS on STN  
TI Comparing the properties of Escherichia coli branching enzyme and  
maize branching enzyme  
AB Escherichia coli glycogen branching enzyme (GBE) and  
maize starch branching enzymes I (SBEI) and II (SBEII)  
were expressed in E. coli and purified. E. coli GBE branched  
amylose at a higher rate than did SBEII, but branched amylose at a lower  
rate than did SBEI. Similar to SBEI, GBE branched amylopectin at a lower  
rate than did SBEII. High-performance anion-exchange chromatog. anal. of  
the branched products produced by BE revealed the min. chain length (cl)  
required for branching. While GBE and SBEII showed the same min. cl [d.p.  
(dp) 12] required for branching, SBEI had a slightly higher min. cl (dp  
16) requirement for branching. The major differences between GBE and SBE  
are their specificities in terms of the size of chains transferred. In  
comparison with SBE, GBE had a much narrower size range of chains  
transferred and transferred mainly shorter chains. While SBEI and SBEII  
produced a large number of chains ranging from dp 6 to over dp 30, GBE

predominantly transferred chains ranging from dp 5 to 16 and produced only a very small number of long chains with dp greater than 20. Although it has been reported that SBEI and SBEII preferentially transfer longer and shorter chains, resp. (1), this study further defines the differences between SBEI and SBEII in the size of chains transferred. SBEI predominantly transfers longer chains with dp greater than 10, while producing few shorter chains with dp 3 to 5. In contrast, SBEII preferentially transfers smaller chains with dp 3 to 9, with the most abundant chains being dp 6 and 7. The significance of min. chain-length requirement by SBE is discussed in setting the invariant size of amylopectin cluster size (9 nm).

AN 1997:347385 HCAPLUS <<LOGINID::20100610>>

DN 127:46831

OREF 127:8835a,8838a

TI Comparing the properties of Escherichia coli branching enzyme and maize branching enzyme

AU Guan, Hanping; Li, Ping; Imparl-Radosevich, Jennifer; Preiss, Jack; Keeling, Peter

CS ExSeed Genetics, Agronomy Dep., Iowa State Univ., Ames, IA, 50011, USA

SO Archives of Biochemistry and Biophysics (1997), 342(1), 92-98

CODEN: ABBIA4; ISSN: 0003-9861

PB Academic

DT Journal

LA English

OSC.G 43 THERE ARE 43 CAPLUS RECORDS THAT CITE THIS RECORD (43 CITINGS)

RE.CNT 28 THERE ARE 28 CITED REFERENCES AVAILABLE FOR THIS RECORD

ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 21 OF 33 HCAPLUS COPYRIGHT 2010 ACS on STN

TI Isolation, characterization and expression analysis of a starch branching enzyme II cDNA from wheat

AB A full-length cDNA (2970 bp) encoding a starch branching enzyme II (SBEII; EC 2.4.1.18) in wheat (Triticum aestivum L. cv Fielder) kernel was isolated from a cDNA library. The translated region of the cDNA predicted a 823 amino acid primary product with a mol. mass of 91.4 kDa. A 54 amino acid transit peptide was postulated to be cleaved from the pre-protein to give a 769 amino acid (85.4 kDa) mature polypeptide, which showed extensive sequence similarity to SBEII sequences characterized from maize, rice and pea. Expression of the isolated cDNA in a BE-deficient E. coli strain demonstrated that it encoded a functional BE. RNA anal. of Sbe2 gene expression during seed development revealed that Sbe2 mRNA levels were highest in young kernels (5-10 days post-anthesis) and declined as the kernels matured.

AN 1997:123840 HCAPLUS <<LOGINID::20100610>>

DN 126:248817

OREF 126:48055a,48058a

TI Isolation, characterization and expression analysis of a starch branching enzyme II cDNA from wheat

AU Nair, Ramesh B.; Baga, Monica; Scoles, Graham J.; Kartha, Kutty K.; Chibbar, Ravindra N.

CS Department of Crop Science and Plant Ecology, University of Saskatchewan, Saskatoon, SK, S7N 5A8, Can.

SO Plant Science (Shannon, Ireland) (1997), 122(2), 153-163

CODEN: PLSCE4; ISSN: 0168-9452

PB Elsevier

DT Journal

LA English

OSC.G 30 THERE ARE 30 CAPLUS RECORDS THAT CITE THIS RECORD (30 CITINGS)

L12 ANSWER 22 OF 33 HCAPLUS COPYRIGHT 2010 ACS on STN



TI Differential expression and properties of starch-  
branching enzyme isoforms in developing wheat endosperm

AB Three forms of starch-branching enzyme (BE)  
from developing hexaploid wheat (*Triticum aestivum*) endosperm have been  
partially purified and characterized. Immunol. cross-reactivities  
indicate that two forms (WBE-IAD, 88 kDa, and WBE-IB, 87 kDa) are related  
to the maize BE I class and that WBE-II (88 kDa) is related to  
maize BE II. Comparison of the N-terminal sequences from WBE-IAD  
and WBE-II with maize and rice BEs confirms these relationships.  
Evidence is presented from the anal. of nullisomic-tetrasomic wheat lines  
demonstrating that WBE-IB is located on chromosome 7B and that the WBE-IAD  
fraction contains polypeptides that are encoded on chromosomes 7A and 7D.  
The wheat endosperm BE classes are differentially expressed  
during endosperm development. WBE-II is expressed at a constant  
level throughout mid and late endosperm development. In contrast, WBE-IAD  
and WBE-IB are preferentially expressed in late endosperm  
development. Differences are also observed in the kinetic characteristics of  
the enzymes. The WBE-I isoforms have a 2- to 5-fold higher affinity for  
amylose than does WBE-II, and the WBE-I isoforms are activated up to  
5-fold by phosphorylated intermediates and inorg. phosphate, whereas  
WBE-II is activated only 50%. The potential implications of this  
activation of BE I for starch biosynthesis are discussed.

AN 1997:73618 HCAPLUS <<LOGINID::20100610>>

DN 126:169149

OREF 126:32649a,32652a

TI Differential expression and properties of starch-  
branching enzyme isoforms in developing wheat endosperm

AU Morell, Matthew K.; Blennow, Andreas; Kosar-Hashemi, Behjat; Samuel,  
Michael S.

CS Cooperative Res. Cent. Plant Sci., Canberra, ACT 2601, Australia

SO Plant Physiology (1997), 113(1), 201-208

CODEN: PLPHAY; ISSN: 0032-0889

PB American Society of Plant Physiologists

DT Journal

LA English

OSC.G 90 THERE ARE 90 CAPLUS RECORDS THAT CITE THIS RECORD (90 CITINGS)

L12 ANSWER 23 OF 33 HCAPLUS COPYRIGHT 2010 ACS on STN

TI Evolutionary conservation and expression patterns of  
maize starch branching enzyme I and  
IIb genes suggest isoform specialization

AB Expression of the maize (*Zea mays* L.) starch  
branching enzyme (SBE) genes Sbe1 and Sbe2 were  
characterized during kernel development and in vegetative tissues. The  
onset of Sbe1 and Sbe2 expression during endosperm development  
was similar to that of other genes involved in starch biosynthesis (Wx,  
Sh2 and Bt2). However, the expression of Sbe2 peaked earlier  
than that of Sbe1 in developing endosperm and embryos resulting in a shift  
in the ratio of Sbe1 to Sbe2 relative message levels during kernel and  
embryo development. Transcripts hybridizing to the Sbe2 probe were not  
detectable in leaves kernel and embryo development. Transcripts  
hybridizing to the Sbe2 probe were not detectable in leaves or roots which  
nonetheless have SBEII enzymic activity, suggesting that there may be  
another divergent SBEII-like gene(s) in maize. A similar  
expression pattern is shared between the maize genes and  
related genes in pea, which together with their evolutionary conservation,  
suggests that the SBE isoforms may play unique roles in starch  
biosynthesis during plant development.

AN 1996:466120 HCAPLUS <<LOGINID::20100610>>

DN 125:137991

OREF 125:25725a

TI Evolutionary conservation and expression patterns of  
maize starch branching enzyme I and  
IIb genes suggest isoform specialization  
AU Gao, Ming; Fisher, Dane K.; Kim, Kyung-Nam; Shannon, Jack C.; Gultinan,  
Mark J.  
CS Dep. of Horticulture, Pennsylvania State Univ., University Park, PA,  
16802, USA  
SO Plant Molecular Biology (1996), 30(6), 1223-1232  
CODEN: PMBIDB; ISSN: 0167-4412  
PB Kluwer  
DT Journal  
LA English  
OSC.G 52 THERE ARE 52 CAPLUS RECORDS THAT CITE THIS RECORD (52 CITINGS)

L12 ANSWER 24 OF 33 HCAPLUS COPYRIGHT 2010 ACS on STN  
TI Two closely related cDNAs encoding starch branching  
enzyme from Arabidopsis thaliana  
AB Two starch branching enzyme (SBE) cDNAs were  
identified in an Arabidopsis seedling hypocotyl library using  
maize Sbe1 and Sbe2 cDNAs as probes. The two cDNAs have diverged  
5', and 3' ends, but encode proteins which share 90% identity over an  
extensive region with 70% identity to maize SBE IIb. Genomic  
Southern blots suggest that the two cDNAs are the products of single,  
independent genes, and that addnl., more distantly related SBE genes may  
exist in the Arabidopsis genome. The two cDNAs hybridize to transcripts  
which show similar expression patterns in Arabidopsis vegetative  
and reproductive tissues, including seedlings, inflorescence rachis,  
mature leaves, and flowers. This is the first report of the  
identification of cDNAs encoding two closely related starch branching  
enzymes from the same species.  
AN 1996:149142 HCAPLUS <<LOGINID::20100610>>  
DN 124:224561  
OREF 124:41433a,41436a  
TI Two closely related cDNAs encoding starch branching  
enzyme from Arabidopsis thaliana  
AU Fisher, Dane K.; Gao, Ming; Kim, Kyung-Nam; Boyer, Charles D.; Gultinan,  
Mark J.  
CS Dep. Horticulture, Pennsylvania State Univ., Univ. Park, PA, 16802, USA  
SO Plant Molecular Biology (1996), 30(1), 97-108  
CODEN: PMBIDB; ISSN: 0167-4412  
PB Kluwer  
DT Journal  
LA English  
OSC.G 27 THERE ARE 27 CAPLUS RECORDS THAT CITE THIS RECORD (27 CITINGS)

L12 ANSWER 25 OF 33 HCAPLUS COPYRIGHT 2010 ACS on STN  
TI Allelic analysis of the maize amylose-extender locus suggests  
that independent genes encode starch-branching enzymes IIa and IIb  
AB Starch branching enzymes (SBE) catalyze the formation of  
 $\alpha$ -1,6-glucan linkages in the biosynthesis of starch. Three distinct  
SBE isoforms have been identified in maize (*Zea mays* L.)  
endosperm, SBEI, IIa, and IIb. Independent genes have been identified  
that encode maize SBEI and IIb; however, it has remained  
controversial as to whether SBEIIa and IIb result from  
post-transcriptional processes acting on the product of a single gene or  
whether they are encoded by sep. genes. Thus, 16-isogenic lines carrying  
independent alleles of the maize amylose-extender (ae) locus,  
the structural gene for SBEIIb, were analyzed. At 22 days after  
pollination ae-B1 endosperm expressed little She2b  
(ae)-hybridizing transcript, and as expected, ae-B1 endosperm also lacked  
detectable SBEIIb enzymic activity,. Also, ae-B1 endosperm contained

SBEIIa enzymic activity, strongly supporting the hypothesis that endosperm SBEIIa and IIb are encoded by sep. genes. Furthermore, addition to encoding the predominant Sbe2b-hybridizing message expressed in endosperm, the ae gene also encodes the major She2b-like transcript expressed in developing embryos and tassels.

AN 1996:119513 HCAPLUS <<LOGINID::20100610>>

DN 124:170828

OREF 124:31587a,31590a

TI Allelic analysis of the maize amylose-extender locus suggests that independent genes encode starch-branching enzymes IIa and IIb

AU Fisher, Dane K.; Gao, Ming; Kim, Kyung-Nam; Boyer, Charles D.; Gultinan, Mark J.

CS Biotechnol. Inst., Pennsylvania State Univ., University Park, PA, 16802, USA

SO Plant Physiology (1996), 110(2), 611-19

CODEN: PLPHAY; ISSN: 0032-0889

PB American Society of Plant Physiologists

DT Journal

LA English

OSC.G 39 THERE ARE 39 CAPLUS RECORDS THAT CITE THIS RECORD (39 CITINGS)

L12 ANSWER 26 OF 33 HCAPLUS COPYRIGHT 2010 ACS on STN

TI Starch branching enzymes belonging to distinct enzyme families are differentially expressed during pea embryo development

AB CDNA clones for two isoforms of starch branching enzyme (SBEI and SBEII) have been isolated from pea embryos and sequenced. The deduced amino acid sequences of pea SBEI and SBEII are closely related to starch branching enzymes of maize, rice, potato and cassava and a number of glycogen branching enzymes from yeast, mammals and several prokaryotic species. In comparison with SBEI, the deduced amino acid sequence of SBEII lacks a flexible domain at the N-terminus of the mature protein. This domain is also present in maize SBEII and rice SBEIII and resembles one previously reported for pea granule-bound starch synthase II (GBSSII). However, in each case it is missing from the other isoform of SBE from the same species. On the basis of this structural feature (which exists in some isoforms from both monocots and dicots) and other differences in sequence, SBEs from plants may be divided into two distinct enzyme families. There is strong evidence from our own and other work that the amylopectin products of the enzymes from these two families are qual. different. Pea SBEI and SBEII are differentially expressed during embryo development. SBEI is relatively highly expressed in young embryos while maximum expression of SBEII occurs in older embryos. The differential expression of isoforms which have distinct catalytic properties means that the contribution of each SBE isoform to starch biosynthesis changes during embryo development. Qual. measurement of amylopectin from developing and maturing embryos confirms that the nature of amylopectin changes during pea embryo development and that this correlates with the differential expression of SBE isoforms.

AN 1995:459734 HCAPLUS <<LOGINID::20100610>>

DN 123:136225

OREF 123:24081a,24084a

TI Starch branching enzymes belonging to distinct enzyme families are differentially expressed during pea embryo development

AU Burton, Rachel A.; Bewley, J. Derek; Smith, Alison M.; Bhattacharyya, Madan K.; Tatge, Helma; Ring, Steve; Bull, Vicky; Hamilton, William D. O.; Martin, Cathie

CS John Innes Centre, John Innes Institute, Norwich, NR4 7UH, UK

SO Plant Journal (1995), 7(1), 3-15

CODEN: PLJUED; ISSN: 0960-7412

DT Journal

LA English

OSC.G 91 THERE ARE 91 CAPLUS RECORDS THAT CITE THIS RECORD (91 CITINGS)

L12 ANSWER 27 OF 33 HCAPLUS COPYRIGHT 2010 ACS on STN

TI Expression of branching enzyme II of maize endosperm  
in *Escherichia coli*

AB A cDNA clone encoding maize branching enzyme II (BEII) has been independently isolated from a maize endosperm cDNA library. The deduced protein sequence of maize BEII was compared with that of BE from diverse sources. The gene encoding mature BEII of maize endosperm has been expressed in *E. coli* using the T7 promoter. The expressed BEII was purified to near homogeneity so that amylolytic activity and bacterial BE could be completely eliminated from the BE preparation. The expressed enzyme showed very similar properties to those of bEII purified from developing maize endosperm. This result confirmed our earlier report that BEII had a lower rate of branching amylose and the rate of branching amylopectin was twice that of branching amylose. This study also showed a greater advantage of purifying BEII from the bacterial expression system than from developing maize endosperm. Most importantly, this study has established a useful tool to study the structure-function relationships of the maize BE using site-directed mutagenesis.

AN 1995:140589 HCAPLUS <<LOGINID::20100610>>

DN 123:4386

OREF 123:915a,918a

TI Expression of branching enzyme II of maize endosperm  
in *Escherichia coli*

AU Guan, Han Ping; Baba, Tadashi; Preiss, Jack

CS Department Biochemistry, Michigan State University, East Lansing, MI,  
48824, USA

SO Cellular and Molecular Biology (Paris) (1994), 40(7), 981-8  
CODEN: CMOBEF; ISSN: 0145-5680

PB C.M.B. Association

DT Journal

LA English

OSC.G 24 THERE ARE 24 CAPLUS RECORDS THAT CITE THIS RECORD (24 CITINGS)

L12 ANSWER 28 OF 33 HCAPLUS COPYRIGHT 2010 ACS on STN

TI Genetic isolation, cloning, and analysis of a Mutator-induced, dominant  
antimorph of the maize amylose extender1 locus

AB The authors report the genetic identification, mol. cloning, and characterization of a dominant mutant at the amylose extender1 locus, Ael-5180. The identities of the authors' clones are corroborated by their ability to reveal DNA polymorphisms between seven wild-type revertants from Ael-5180 relative to the Ael-5180 mutant allele and between four of five independently derived, Mutator (Mu)-induced recessive ael alleles relative to their resp. wild-type progenitor alleles. The Ael-5180 mutation is associated with two *Mul* insertions flanked by complex rearrangements of ael-related sequences. One of the *Mul* elements is flanked by inverted repeats of ael-related DNA of at least 5.0 kb in length. This *Mul* element and at least some of this flanking inverted repeat DNA are absent or hypermethylated in six of seven wild-type revertants of Ael-5180 that were analyzed. The second *Mul* element is flanked on one side by the 5.0-kb ael-specific repeat and on the other side by a sequence that does not hybridize to the ael-related repeat sequence. This second *Mul* element is present in revertants to the wild type and does not, therefore, appear to affect ael gene function. A 2.7-kb ael transcript can be detected in wild-type and homozygous ael-Ref endosperms 20 days after pollination. This transcript is absent in endosperms containing one, two, or three doses of Ael-5180. This result is consistent with a suppression model to explain the dominant gene action of

Ael-5180 and establishes Ael-5180 as an antimorphic allele. Homozygous wild-type seedlings produce no detectable transcript, indicating some degree of tissue specificity for ael expression. Sequence analyses establish that ael encodes starch branching enzyme II.

AN 1994:550052 HCAPLUS <<LOGINID::20100610>>

DN 121:150052

OREF 121:26949a,26952a

TI Genetic isolation, cloning, and analysis of a Mutator-induced, dominant antimorph of the maize amylose extender1 locus

AU Stinard, Philip S.; Robertson, Donald S.; Schnable, Patrick S.

CS Dep. Agron., Iowa State Univ., Ames, IA, 50011, USA

SO Plant Cell (1993), 5(11), 1555-66

CODEN: PLCEEW; ISSN: 1040-4651

DT Journal

LA English

OSC.G 62 THERE ARE 62 CAPLUS RECORDS THAT CITE THIS RECORD (62 CITINGS)

L12 ANSWER 29 OF 33 HCAPLUS COPYRIGHT 2010 ACS on STN

TI Modulating the quantity and quality of starch synthesis in plants by placing the gene for a starch-metabolizing enzyme under control of a regulated promoter

AB A method of producing a plant with switchable starch-synthesizing ability by stably incorporating a target gene for an enzyme involved in a starch or glycogen biosynthetic pathway and under the control of a regulated promoter into the genome of a recipient plant. A plant with controllable starch-synthesizing ability may have switchable starch yield, and/or switchable starch quality. Starch or glycogen biosynthetic enzymes include soluble starch synthase, branching enzyme, glycogen synthase, ADP-glucose pyrophosphorylase, self-glucosylating protein, glycogenin and amylogenin. DNA constructs for use in this method are described, as well as plants transformed with said DNA constructs, the seeds and progeny of such plants, and hybrids whose pedigree includes such plants. The examples demonstrate the functioning of the chemical-inducible promoter of the gene for the 27 kd subunit of glutathione-S-transferase II in maize endosperm and discuss the construction of appropriate expression vectors.

AN 1994:530242 HCAPLUS <<LOGINID::20100610>>

DN 121:130242

OREF 121:23445a,23448a

TI Modulating the quantity and quality of starch synthesis in plants by placing the gene for a starch-metabolizing enzyme under control of a regulated promoter

IN Keeling, Peter Lewis

PA Zeneca Ltd., UK

SO PCT Int. Appl., 52 pp.

CODEN: PIXXD2

DT Patent

LA English

FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
	-----	----	-----	-----	-----
PI	WO 9411520	A2	19940526	WO 1993-GB2305	19931109 <--
	WO 9411520	A3	19940804		
	W: AU, BB, BG, BR, BY, CA, CZ, FI, HU, JP, KP, KR, KZ, LK, LV, MG, MN, MW, NO, NZ, PL, RO, RU, SD, SK, UA, US, VN				
	RW: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG				
	AU 9454285	A	19940608	AU 1994-54285	19931109 <--
PRAI	GB 1992-23454	A	19921109	<--	
	WO 1993-GB2305	W	19931109	<--	

OSC.G 22 THERE ARE 22 CAPLUS RECORDS THAT CITE THIS RECORD (22 CITINGS)  
RE.CNT 10 THERE ARE 10 CITED REFERENCES AVAILABLE FOR THIS RECORD  
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 30 OF 33 HCAPLUS COPYRIGHT 2010 ACS on STN

TI Expression of branching enzyme I of maize endosperm in  
Escherichia coli

AB The gene encoding for mature branching enzyme (BE) I (BEI) of  
maize (*Zea mays* L.) endosperm has been expressed in  
*Escherichia coli* using the T7 promoter. The expressed BEI was  
purified to near homogeneity so that amylolytic activity and bacterial BE  
could be completely eliminated from the BE preparation. The recombinant enzyme  
showed properties very similar to those of BEI purified from developing  
maize endosperm with respect to branching amylose and amylopectin.  
This result confirmed the authors' earlier report that maize  
endosperm BEI had a higher rate of branching amylose and a much lower rate  
(less than 10% of that of branching amylose) of branching amylopectin.  
This study also showed a great advantage in purifying BE from the  
bacterial expression system rather than from developing  
maize endosperm. Most important, this study has established the  
system with which to study the structure-function relationships of the  
maize BEI using site-directed mutagenesis.

AN 1994:502618 HCAPLUS <<LOGINID::20100610>>

DN 121:102618

OREF 121:18339a,18342a

TI Expression of branching enzyme I of maize endosperm in  
*Escherichia coli*

AU Guan, Han Ping; Baba, Tadashi; Preiss, Jack

CS Dep. Biochem., Michigan State Univ., East Lansing, MI, 48824, USA

SO Plant Physiology (1994), 104(4), 1449-53

CODEN: PLPHAY; ISSN: 0032-0889

DT Journal

LA English

OSC.G 31 THERE ARE 31 CAPLUS RECORDS THAT CITE THIS RECORD (31 CITINGS)

L12 ANSWER 31 OF 33 HCAPLUS COPYRIGHT 2010 ACS on STN

TI Comparison of soluble starch synthases and branching enzymes from leaves  
and kernels of normal and amylose-extender maize

AB Soluble starch synthases (SS) and branching enzymes (BE) from 20-day-old  
maize leaves and 22-day-old seeds of normal and amylose-extender  
(ae) were purified by DEAE-cellulose chromatog. Elution profiles of leaf  
exts. showed 1 major SS and 2 BE fractions from both genotypes. The SS  
fractions from normal and ae leaf exts. were capable of citrate-stimulated  
starch synthesis and had different reaction rates with various primers.  
The 2 BE fractions from normal leaf exts. differed significantly from each  
other but not when compared to the same BE from ae. Comparison of BE  
fractions from ae and normal leaves showed no differences based on  
chromatog., kinetic, and immunol. properties. Comparison of the leaf  
enzymes with endosperm enzymes showed major differences. Leaf exts. did  
not contain SSII or BEIIb observed in endosperm exts. Developing ae  
endosperm lacked BEIIb activity and ae was the structural gene for BEIIb.  
The tissue-specific expression of BEIIb in the endosperm  
provided the basis for explaining the tissue-specific expression  
of ae. It was proposed that as BEIIb is expressed in the  
endosperm, but not leaves, allelic substitution at the ae locus modifies  
only endosperm starch synthesis.

AN 1990:94355 HCAPLUS <<LOGINID::20100610>>

DN 112:94355

OREF 112:15955a,15958a

TI Comparison of soluble starch synthases and branching enzymes from leaves  
and kernels of normal and amylose-extender maize

AU Dang, Peter L.; Boyer, Charles D.  
CS Dep. Hort., Pennsylvania State Univ., University Park, PA, 16802, USA  
SO Biochemical Genetics (1989), 27(9-10), 521-32  
CODEN: BIGEBA; ISSN: 0006-2928  
DT Journal  
LA English  
OSC.G 7 THERE ARE 7 CAPLUS RECORDS THAT CITE THIS RECORD (7 CITINGS)

L12 ANSWER 32 OF 33 HCAPLUS COPYRIGHT 2010 ACS on STN

TI Maize leaf and kernel starch synthases and starch branching  
enzymes

AB Soluble starch synthases and branching enzymes were partially purified from developing leaves and kernels of maize using DEAE-cellulose chromatog. One form of starch synthase and 2 forms of branching enzyme were detected in leaves as compared to 2 forms of starch synthase and 3 forms of branching enzyme isolated from the kernels. The starch synthase fraction from the leaves and the 1st starch synthase fraction from the kernels showed greater activity in reactions containing various glycogens as primers than in those containing amylopectin. In addition, both were capable

of synthesizing a polyglucan in the absence of an added primer but in the presence of Na citrate and bovine serum albumin (citrate-stimulated starch synthesis). The 2nd starch synthase fraction from kernels showed greater activity with amylopectin as primer and had no citrate-stimulated activity. The leaf enzyme and endosperm starch synthase I are suggested to be the same enzyme and constitutively expressed. Branching enzymes from leaves and kernels differed not only in their elution profiles but also their stimulation of phosphorylase a (assay A) and amylose branching (assay B) activities. A minor branching enzyme fraction from leaves (leaf branching enzyme I) eluted from the DEAE-cellulose column after the addition of a salt gradient, whereas branching enzyme I from kernels eluted in the buffer wash prior to the application of the gradient. However, the ratios of assay A to assay B suggested that branching enzyme I from leaves was catalytically similar to branching enzyme I from the kernels. The major leaf branching enzyme (branching enzyme II) eluted at the same position from the DEAE-cellulose column as endosperm branching enzyme IIa. These enzymes had similar ratios of activity (assay A/assay B). The cross-reaction of leaf branching enzymes with antisera prepared against maize endosperm branching enzymes in immunodiffusion expts. and enzyme activity neutralization expts. further demonstrated the relationship of the leaf and endosperm branching enzymes.

AN 1988:434288 HCAPLUS <<LOGINID::20100610>>

DN 109:34288

OREF 109:5733a,5736a

TI Maize leaf and kernel starch synthases and starch branching  
enzymes

AU Dang, Peter L.; Boyer, Charles D.

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OSC.G 20 THERE ARE 20 CAPLUS RECORDS THAT CITE THIS RECORD (20 CITINGS)

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TI Evidence for independent genetic control of the multiple forms of  
maize endosperm branching enzymes and starch synthases

AB Soluble starch synthase and starch-branching enzymes in exts. from kernels of 4 corn genotypes were compared. Exts. from normal (nonmutant) corn were found to contain 2 starch synthases and 3 branching

enzyme fractions. The different fractions could be distinguished by chromatog. properties and kinetic properties under various assay conditions. Kernels homozygous for the recessive amylose-extender (ae) allele were missing branching enzyme IIb. In addition, the citrate-stimulated activity of starch synthase I was reduced. This activity could be regenerated by the addition of branching enzyme to this fraction. No other starch synthase fractions were different from normal enzymes. Exts. from kernels homozygous for the recessive dull (du) allele were found to contain lower branching enzyme IIa and starch synthase II activities. Other fractions were not different from the normal enzymes. Anal. of exts. from kernels of the double mutant ae du indicated that the 2 mutants act independently. Branching enzyme IIb was absent and the citrate-stimulated reaction of starch synthase I was reduced but could be regenerated by the addition of branching enzyme (ae properties) and both branching enzyme IIa and starch synthase II were greatly reduced (du properties). Starch from ae and du endosperms contains higher amylose (66 and 42%, resp.) than normal endosperm (26%). In addition, the amylopectin fraction of ae starch is less highly branched than amylopectin from normal or du starch. The above observations suggest that the alterations of the starch may be accounted for by changes in the soluble synthase and branching enzyme fractions.

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TI Evidence for independent genetic control of the multiple forms of maize endosperm branching enzymes and starch synthases

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